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Minimum
Maximum
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                 Database :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Title:
Perfect score:
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                                                                                                                                                                                                                                                         seq length: 0
seq length: 2000000000
                                                                                        A Geneseq 16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
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1047
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geneseqp2003as:*
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                                                                                                                                                                                                                                                                                                                                                   386760381 residues
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and is No. is the number of results predicted by chance to have a greater than or equal to the score of the result being printed, s derived by analysis of the total score distribution.

### SUMMARIES

25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	89	7	6	υı	4	u	2	1	No.	Result
945.5	945.5	945.5	945.5	945.5	948	975	975	975	975	975	975	975	1011	1036.5	1036.5	1047	1047	1047	1047	1047	1047	. 1047	1047	1047	Score	
90.3	90.3	90.3	90.3	90.3	90.5	93.1	93.1	93.1	93.1	93.1	93.1	93.1	96.6	99.0	99.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0		Ouerv
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Adm83852 Human can	Adm83853 Human can	Adm83801 Human can	Adm83808 Human can	Add84545 121P1F1 v	-	Adm83858 Human can	Adm83809 Human can	Adm83803 Human can	Adm83859 Human can	Adm83857 Human can	Add84547 121P1F1 v	Aam40043 Human pol	Adm83814 Human can	Adm83835 Human can	Adm83834 Human can	Abp75541 Human sec	Adm83804 Human can	Adm83811 Human can	Adm83793 Human can	Adm83812 Human can	Adm83810 Human can	Adm83851 Human can	Adj70015 Human hea	7 121P1F	Description	

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135.5	255.5	287	329.5	349	465	465	465	465	584	584	584	584	591	591	591	591	591	909	614
12.9	24.4	27.4	31.5	33.3	44.4	44.4	44.4	44.4	55.8	55.8	55.8	55.8	56.4	56.4	56.4	56.4	56.4	57.9	58.6
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ADP26646	ADH32846	AAG74669	ABG12341	ADM83815	ADM83805	ADM83795	ADM83836	ADD84539	ADM83837	ADM83806	ADM83797	ADD84541	ADM83844	ADM83807	ADM83845	ADM83799	ADD84543	AAM41829	ADM83843
Adp26646	Adh32846	Aag74669	Abg12341	Adm83815	Adm83805	Adm83795	Adm83836	Add84539	Adm83837	Adm83806	Adm83797	Add84541	Adm83844	Adm83807	Adm83845	Adm83799	Add84543	Aam41829	Adm83843
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# ALIGNMENTS

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RESULT 1
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ID ADD84
XX ADB8
XX ADB8
XX ADB8
XX I21E
XX I21E
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XX W02(
XX Example I21
XX ADB8
PF 28-1
XX AD86
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XX AD86
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XX I21E
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121P1F1; 121P1F1 modulation; human; chromosome 4q; cytostatic; gene therapy; vaccine; cancer; immune response; immunisation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADD84537;
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Composition comprising a substance that modulates the status of 121P1F1, useful in diagnosing, preventing, prognosticating or treating patients with cancer that expresses 121P1F1, such as breast, colon, ovarian or lung cancer. WPI; 2003-156757/15. N-PSDB; ADD84536. Jakobovits

Challita-Eid PM, Hubert

RS,

Raitano AB,

Faris Σ,

Afar

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Claim 19; Fig 2A; 285pp; English.

The present invention describes a composition (I) comprising a substance that modulates the status of 121PIF1 (gene and encoded protein), or a molecule that is modulated by 121PIF1, where the status of a cell that expresses 121PIF1 is modulated. The human 121PIF1 gene maps to chromosome 4q. (I) has cytostatic activity, and can be used in gene therapy, and in vaccines. The composition (I) can be used for diagnosing, preventing, prognosticating or treating patients with cancer that expresses 121PIF1, such as breast, colon, ovarian or lung cancer. The 121PIF1 gene or its fragment can be used to elicit a humoral or cellular immune response.

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RESULT 2
ADJ70015
ID ADJ7
XX ADJ7
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                                                                      Identifying a mitochondrial target for drug screening assays and treating diseases associated with altered mitochondrial function, comprises detecting a modified polypeptide in a sample and correlative detection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mitochondrial; human; screening assay; diabetes mellitus; Huntington's disease; osteoarthritis; Leber's hereditary optic neuropathy; LHON; mitochondrial encephalopathy lactic acidosis and stroke; MELAS;
                                                                                                                                                                                                                                                                                                                                                                              12-APR-2002; 2002US-0372843P.
17-JUN-2002; 2002US-0389987P.
20-SEP-2002; 2002US-0412418P.
     Claim
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(BUCK-) BUCK INST AGE
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RESULT 3
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AC ADM8
AC ADM8
AC ADM8
AC Huma
AC Huma
AC Huma
AC COLC
KW COLC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Sin
Matches 205;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; cancer gene 121PIF1; cytostatic; cancer; chromosome 4q; HI human leukocyte antigen; prostate cancer; bladder cancer; kidney colon cancer; lung cancer; pancreatic cancer; breast cancer; cervical cancer; stomach cancer; gene therapy; vaccine.
                                                                                    (FARI/)
(AFAR/)
                                                                                                                                          (CHAL/)
(HUBE/)
(RAIT/)
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                                                                                                                                                                                                                                                                                                                         28-FEB-2002; 2002US-00087190
                                                                                                                                                                                                                                                                                                                                                                                   04-DEC-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human cancer gene 121P1F1 protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181
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                                                      FARIS M.
AFAR D E H.
GE W.
                                                                                                                                                                                                       CHALLITA-EID P M.
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Pred. No. 1.5
); Mismatches
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Composition comprising the movel composition in a numen unit cose form, a creambinant protein comprising an antigen-binding region of a monoclonal comprising an antibody, a single chain monoclonal antibody, a composition of a monoclonal antibody, a comprising an antibody a single chain monoclonal antibody the variable domains of the heavy and light chains of a monoclonal comprising a polynucleotide that encodes a single chain monoclonal antibody, a vector comprising a polynucleotide that encodes an analogue chain monoclonal antibody, a polynucleotide that encodes an analogue chain monoclonal antibody, a polynucleotide that encodes an analogue chain monoclonal action to a cell that expresses 121P1F1, inhibiting growth of cancer cells that expresses (121P1F1) (comprising administering to the cells the composition), treating a patient who bears cancer cells that express 121P1F1, generating a patient who has or who is suspected to 121P1F1, inducing an immune cresponse directed to 121P1F1, inducing an immune cresponse of cancer in an individual and an assay for detecting the presence of a 121P1F1-related protein or polynucleotide in a biological sample from a comprise a polynucleotide that comprises a 121P1F1-related protein or polynucleotide in a biological composition may comprise a polynucleotide that comprises a 121P1F1-related protein or polynucleotide in a biological composition cading sequence provided that the coding sequence does not encode the entire amino acid sequence of 121P1F1 (ADM83793. The substance also comprises a polynucleotide that encodes at least one peptide given in 16 Tables (given in the specification), the peptides peptide variants. The composition is useful for detecting, treating or its splice variants. The composition is useful for detecting, treating or its splice variants of the present cancer. The composition can also be used as a vaccine to treat or prevent cancer. The composition can also be used as a vaccine to treat or prevent cancer that expresses or overexpresses calculated to t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New composition comprising a substance that modulates the status of 121P1F1 or a molecule that is modulated by 121P1F1, useful for detecting, treating or preventing cancer e.g. prostate, bladder, colon, breast or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Jakobovits
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 205 AA;
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cancer.
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181
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                                                                                                                                                                                                   TRLAKELSSLRDOREOLKAEVEKYKDCDPOVVEEIROANKVAKEAANRWTDNIFAIKSWA 180
                                                                      KRKFGFEENKIDRTFGIPEDFDYID 205
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                                                                                                                                                                                                                                                                                                                                                                                                                     MSKKKGLSAEEKRTRMMEIFSETKDVFQLKDLEKIAPKEKGITAMSVKEVLQSLVDDGMV
                                                                                                                                    TRLAKELSSLRDQREQLKAEVEKYKDCDPQVVEEIRQANKVAKEAANRWTDNI FAIKSWA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 1047; DB 8;
Pred. No. 1.5e-88;
0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (full-length or fragment).
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RESULT 4 ADM83810

preferably prostate cancer,

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The invention relates to a composition comprising a substance that CC gene) or a molecule that is modulated by 121PIPI where status of the cell that expressed sets 121PIPI is modulated. Also included are a pharmaceutical cc composition comprising the novel composition in a human unit dose form, a crecombinant protein comprising an antipody, a mon-human transgenic animal that produces an antibody, a contribody, a non-human transgenic animal that produces an antibody at that immunospecifically binds to a 121PIF1-related protein (comprising the variable domains of the heavy and light chains of a monoclonal comprising a cytotoxic agent or a diagnostic agent to a cell that expresses 121PIF1 (comprising a cytotoxic agent or a diagnostic agent to a cell that expresses 121PIF1, inhibiting growth of cancer cells that expresses cc 121PIF1 (comprising administering to the cells the composition), treating a patient who has or who is suspected to 121PIF1, generating a patient who has or who is suspected of having cancer, monitoring the composition may comprise a polymucleotide that comprises the composition may comprise a polymucleotide that comprises a 121PIF1 composition may comprise a polymucleotide that comprise a cell composition may comprise a polymucleotide that comprises a 121PIF1 composition may comprise a polymucleotide that comprises a 121PIF1 composition may comprise a polymucleotide that the coding sequence does not encode the entire amino acid sequence of 121PIF1 (ADM83793. The spidle given in 16 Tables (given in the specification), the peptides being HIA (human leukocyte antigen)-binding epitopes from 121PIF1 or its spidle variants. The composition is useful for detecting, treating or its spidle variants. The composition is useful for detecting, treating or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               human leukocyte antigen; prostate cancer; bladder cancer; kidney cancer; colon cancer; lung cancer; pancreatic cancer; breast cancer; cervical cancer; stomach cancer; gene therapy; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New composition comprising a substance that modulates the status of 121P1F1 or a molecule that is modulated by 121P1F1, useful for detecting, treating or preventing cancer e.g. prostate, bladder, colon, breast or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (HUBE/)
(RAIT/)
(FARI/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; cancer gene 121P1F1; cytostatic; cancer; chromosome
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JAKOBOVITS A.
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HUBERT R S.
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Matches 205;
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                                                                       treating
                                                                                             New composition comprising 121P1F1 or a molecule that
                                                                                                                                                                    WPI; 2004-060522/06
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Jakobovits A;
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(HUBE/)
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HUBERT R S.
RAITANO A B.
FARIS M.
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                                                                         cancer
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                                                                  a substance that modulates the status of is modulated by 121P1F1, useful for detecting. cer e.g. prostate, bladder, colon, breast or
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Disclosure;

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211pp; English

RESULT 6 ADM83793

ADM83793

standard;

protein;

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Human 03-JUN-2004

cancer

gene (first

121P1F1 protein

#1.

Human; cancer gene 121P1F1; cytostatic; cancer; chromosome 4q; human leukocyte antigen; prostate cancer; bladder cancer; kidn colon cancer; lung cancer; pancreatic cancer; breast cancer;

kidney

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Continuing process completes by an antibody, a mithody, a concluded that immunospecifically binds to a 121PIF1-related protein (comprising the wariable domains of the heavy and light chains of a monclonal antibody cantibody), a vector comprising a polynucleotide that encodes an analogue contain monoclonal antibody, a vector comprising a polynucleotide that encodes an analogue contain monoclonal antibody, a polynucleotide that encodes an analogue contain monoclonal antibody, a polynucleotide that encodes an analogue contain monoclonal antibody, a polynucleotide that encodes an analogue contain monoclonal antibody, a polynucleotide that encodes an analogue contain monoclonal actions a cytotoxic agent or a diagnostic agent to a cell chair expresses 121PIF1 (comprising administering growth of cancer cells that expresses 121PIF1 (composition), treating contains an analogue contains an analogue contains an analogue contains an antibody, a patient who bears cancer cells that express 121PIF1, generating a commandation monitoring 121PIF1 gene products in a biological sample from a patient who has or who is suspected of having cancer, monitoring the composition may comprise a polynucleotide that comprises a 121PIF1 composition may comprise a polynucleotide that comprises a 121PIF1 composition and concer in an individual and an assay for detecting the composition may comprise a polynucleotide that comprises a 121PIF1 composition and concer is an analogue does not encode the entire amino acid sequence of 121PIF1 (ADM83793). The generative antipan and concer is an analogue of its splice variants. The composition is useful for detecting, treating or its splice variants. The composition is useful for detecting, treating or its splice concer, bladder cancer, kidney cancer, colon cancer, preferably prostate cancer, bladder cancer, kidney cancer, breast cancer, concer, co
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Best Local S
Matches 205
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Pred. No. 1.5e-88;
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cervical cancer;

stomach cancer; gene therapy; vaccine

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CC peptide delivering a cytotycic agent or a diagnostic agent to a cell control of that expresses 121PIF1, inhibiting growth of cancer cells that expresses control of the cells the composition), treating can partient who bears cancer cells that express 12PIFI, generating a commalian immune response directed to 12PIFI, inducing an immune cancer in an individual and an absay for detecting the composition may comprise a polynucleotide that comprise in a biological sample from a comprise a polynucleotide that the coding sequence composition may comprise a polynucleotide that the coding sequence does contenced the entire amino acid sequence of 12PIFI. The generably prostate cancer baseful for detecting the composition may comprises a polynucleotide that the coding sequence does contenced the entire amino acid sequence of 12PIFI (ADM83793). The content of the specification) the peptides content of the given in the specification), the peptides content of the composition is useful for detecting, treating or contenting cancer, preferably prostate cancer, bladder cancer, kidney cancer, colon cancer, lung cancer, pancreatic cancer, bladder cancer, that cancer, concer, concer, concer, concer, concer, cancer that expresses or overexpresses concer, prevent cancer that expresses or overexpresses concer, concer, is a 12PIFI is located on chromosome 4q. The present concer is a 12PIFI protein (full-length or fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gene) or a molecule that is modulated by 121P1F1 where status of the cell that expresses 121P1F1 is modulated. Also included are a pharmaceutical composition comprising the novel composition in a human unit dose form, a recombinant protein comprising an antigen-binding region of a monoclonal antibody, a non-human transgenic animal that produces an antibody, a hybridoma that produces an antibody, a land that produces an antibody that immunospecifically binds to a 121P1F1-related protein (comprising that the companies of the heavy and light chain sof a monoclonal antibody.
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N-PSDB; ADM83792.
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GE W.
JAKOBOVITS A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Raitano
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Query Match Best Local Similarity

Score Pred.

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The invention relates to a composition comprising a substance that modulates the status of 121P1F1 (a protein encoded by a cancer expressed gene) or a molecule that is modulated by 121P1F1 where status of the cell that expresses 121P1F1 is modulated. Also included are a pharmaceutical composition comprising the novel composition in a human unit dose form, a recombinant protein comprising an antigen-binding region of a monoclonal antibody, a non-human transgenic animal that produces an antibody, a hybridoma that produces an antibody, a single chain monoclonal antibody that immunospecifically binds to a 121P1F1-related protein (comprising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; cancer gene 121PIF1; cytostatic; cancer; chromosome 4q; HLA; human leukocyte antigen; prostate cancer; bladder cancer; kidney cancer; colon cancer; lung cancer; pancreatic cancer; breast cancer; cervical cancer; stomach cancer; gene therapy; vaccine.
                                                                                                                                                                                                                                                                                                    Disclosure; SEQ
                                                                                                                                                                                                                                                                                                                                                                                New composition comprising a substance that modulates the status of 121P1F1 or a molecule that is modulated by 121P1F1, useful for detecting, treating or preventing cancer e.g. prostate, bladder, colon, breast or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2004-060522/06
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(HUBE/)
(RAIT/)
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GEW.
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the variable domains of the heavy and light chains of a monoclonal cantibody), a vector comprising a polynucleotide that encodes a single chain monoclonal antibody, a polynucleotide that encodes an analogue peptide, delivering a cytotoxic agent or a diagnostic agent to a cell that expresses 121P1F1 (comprising administering to the cells the composition), treating captaint who bears cancer cells that expresses 121P1F1, generating a composition and commandation immune response directed to 121P1F1, inducing an immune companient who has or who is suspected of having cancer, monitoring the composition may comprise a polynucleotide that comprises a 121P1F1 composition may comprise a polynucleotide that comprises a 121P1F1 composition may comprise a polynucleotide that comprises a 121P1F1 cancer. The composition may comprise a polynucleotide that comprises a 121P1F1 cancer of encode the entire amino acid sequence of 121P1F1 (ADM83793). The composition is useful for detecting, treating or peptide given in 16 Tables (given in the specification), the peptides being HLA (human leukocyte antigen)-binding epitopes from 121P1F1 or cancer, preferably prostate cancer, bladder cancer, kidney cancer, colon cancer, preferably prostate cancer, bladder cancer, kidney cancer, colon cancer, preferably prostate cancer, bladder cancer, kidney cancer, to treat or prevent cancer that expresses or overexpresses concerned to treat or prevent cancer that expresses or overexpresses and the present cancer is slocated on chromosome 4q. The present cancer is concerned to treat or prevent cancer that expresses or overexpresses.
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Best Local :
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leukocyte antigen; prostate cancer; bladder cancer; kidney cancer;
cancer; lung cancer; pancreatic cancer; breast cancer;
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                                                                                                                                                                                                                                                          cancer;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    is a 121P1F1 protein (full-length or fragment).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TRLAKELSSLRDQREQLKAEVEKYKDCDPQVVEEIRQANKVAKEAANRWTDNIFAIKSWA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MSKKKGLSAEEKRTRMMEIFSETKDVFQLKDLEKIAPKEKGITAMSVKEVLQSLVDDGMV
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                                                                                                                                                                                                                                                                                                                                                                                                                gene 121P1F1 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                      stomach cancer; gene therapy; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%;
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Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                                   #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             e 1047; DB 8;
. No. 1.5e-88;
smatches 0;
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Best Loc Matches Query Match

Local

Similarity

ilarity 100.0%; Conservative 0;

Score 1047; Pred. No. 1.5 0; Mismatches

1.5e-88; DB 8;

Indels Length

Gaps

205; <u>,</u>

100.0%;

1 MSKKKGLSAEEKRTRMMEIFSETKDVFQLKDLEKIAPKEKGITAMSVKEVLQSLVDDGMV

MSKKKGLSAEEKRTRYMEIFSETKOVFQLKDLEKIAPKEKGITAMSVKEVLQSLVDDGMV

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120 120

DCERIGTSNYYWAFPSKALHARKHKLEVLESQLSEGSQKHASLQKSIEKAKIGRCETEER DCERIGTSNYYWAFPSKALHARKHKLEVLESQLSEGSQKHASLQKSIEKAKIGRCETEER

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121 61 61 \_

TRLAKELSSLRDQREQLKAEVEKYKDCDPQVVEEIRQANKVAKEAANRWTDNIFAIKSWA 180

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Commodulates the status of 121P1F1 (a protein encoded by a cancer expressed composition or a molecule that is modulated. Also included are a pharmaceutical composition for a molecule that is modulated by 121P1F1 where status of the cell composition or a molecule that is modulated. Also included are a pharmaceutical composition to protein comprising an antipon in a human unit dose form, a recombinant protein comprising an antipon in a human unit dose form, a composition protein comprising an antipon in a human unit dose form, a composition and the produces an antibody, a portion of a monoclonal comprising an antipody, a polymorphism of a monoclonal antibody, a polymorphism of a monoclonal antibody, a polymorphism of a monoclonal expresses (chain monoclonal antibody, a polymorphism of cancer cells that encodes a single chain monoclonal antibody, a polymorphism of cancer cells that expresses 121P1F1, inhibiting growth of cancer, monitoring the composition is unspected of having cancer, monitoring the composition may comprise directed to 121P1F1, inducing an immune response directed to 121P1F1, inducing an immune the composition and an assay for detecting the composition may comprise a polymucleotide that comprises a 121P1F1. The squants of a polymucleotide that coding sequence does composition may comprises a polymucleotide that coding sequence does content of the composition is unspected of having cancer. The composition in 16 Tables (given in the specification), the peptides of peptide given in 16 Tables (given in the specification), the peptides of peptide given in 16 Tables (given in the specification), the peptides of peptide given in 16 Tables (given in the specification), the peptides of cancer, colon cancer, lung cancer, backeted on the composition can also be used as a cancer i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New composition comprising a substance that modulates the status of 121P1F1 or a molecule that is modulated by 121P1F1, useful for detecting, treating or preventing cancer e.g. prostate, bladder, colon, breast or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (CHAL/)
(HUBE/)
(RAIT/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; SEQ ID NO 14; 211pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2004-060522/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Challita-Eid PM, Hubert RS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 08-FEB-2001; 2001US-00779250
Sequence 205
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tung cancer.
                                          sequence is a 121P1F1 protein (full-length or
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AFAR D E H.
GE W.
JAKOBOVITS A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CHALLITA-EID P M.
HUBERT R S.
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                                            fragment).
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29-MAR-2001; 2001US-0280068P.
16-MAY-2001; 2001US-0291280P.
17-MAY-2001; 2001US-0291829P.
17-MAY-2001; 2001US-0291849P.
19-JUN-2001; 2001US-0299478B.
20-JUN-2001; 2001US-0299776P.
20-JUN-2001; 2001US-0300001P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            asthma; Crohn's disease; neurological disorder; epilepsy; cancer; Huntington's disease; Alzheimer's disease; Creutzfeldt-Jakob disease; multiple sclerosis; Parkinson's disease; Cell proliferative disorder; anti-inflammatory; immunosuppressive; neuroprotective; nootropic; neuroleptic; anticonvulsant; cytostatic; antiparkinsonian; anxiolytic; antipsoriatic; antianaemic; anti-HIV; human immunodeficiency virus; secretory polynucleotide; secretory protein.
The invention relates to a secretory polynucleotide (designated sptm) comprising any of 567 polynucleotide sequences (ABZ35837-ABZ36403), a naturally occurring polynucleotide sequence at least 90 % identical to the polynucleotide sequence at least 90 % identical to the golynucleotide sequence at polynucleotide are useful for an RWA equivalent of them. The polynucleotide or polynucleotide are useful for treating, preventing or diagnosing a disease or condition associated with the expression of functional SPTM. These are particularly useful for diagnosing, treating or preventing autoimmune/inflammatory disorders (e.g. acquired immunodeficiency syndrome, anaemia, asthma or Crohn's disease), neurological disorders (e.g. epilepsy, Huntington's disease, dementia, stroke, Alzheimer's disease, Creutzfeldt-Jakob disease,
                                                                                                                                                                                                                                                                                                                                                                          Daffo A, Jones AL, Tran AB, Dahl CR, Gietzeu L, Dufour GE, Hillman JL, Yu JY, Tuason O, Yap PE, Daughtery SC, Dam TC, Liu TF, Nguyen DA, Kleeft Peralta CH, David MH, Lewis SA, Chen AJ, Panze: Flores V, Marwaha R, Lo A, Lan RY, Urashka ME;
                                                                                                                                                                                                                                                            New human secretory proteins and polynucleotides, useful for diagnosing, treating or preventing autoimmune/inflammatory disorders (e.g. AIDS), neurological disorders (e.g. Alzheimer's), or cell proliferations or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human secretory polypeptide SPTM SEQ ID NO 725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABP75541
                                                                                                                                                                                                              Claim 27;
                                                                                                                                                                                                                                                                                                                                      N-PSDB; ABZ35987.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENOMICS INC.
                                                                                                                                                                                                           NO 725; 458pp + Sequence Listing; English.
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Kleefeld Y,
Panzer SR,
                                                                                                                                                                                                                                                                                                                                                                                                                      Amshey SR;
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                                                                                                                                                                                                                                                                                                                   Human; cancer gene 121P1F1; cytostatic; cancer; chromosome 4q; HLA; human leukocyte antigen; prostate cancer; bladder cancer; kidney ca colon cancer; lung cancer; pancreatic cancer; breast cancer;
                                                                                                                                                                                                                                                                                                          cervical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 219
                                                       Challita-Eid
Jakobovits A;
                                                                                                                         (HUBE/)
(RAIT/)
(FARI/)
                                                                                                                                                                                      08-FEB-2001; 2001US-00779250.
                                                                                                                                                                                                                                                            US2003223997-A1
                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                    Human cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                           ADM83834
                                                                                                    (AFAR/)
(GEWW/)
                                                                                                                                                             (CHAL/)
                                                                                          JAKO/)
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                                                                                                   AFAR DEH.
GEW.
                                                                                         JAKOBOVITS
                                                                                                                         RAITANO A B. FARIS M.
                                                                                                                                                             CHALLITA-BID P
                                                                                                                                                   HUBERT R S.
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                                                                                                                                                                                                                                                                                                          cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                         standard; protein; 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KRKFGFEENKIDRTFGIPEDFDYID 205
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TRIAKELSSIRDQREQLKAEVEKYKDCDPQVVEEIRQANKVAKEAANRWTDNIFAIKSWA
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ilarity 100.0%;
Conservative (
                                                                   PM,
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                                                                                                                                                                                                                                                                                                                                                                   gene 121P1F1 variant protein
                                                                                                                                                                                                             2002US-00087190.
                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                           stomach
                                                                    Hubert
                                                                   RS,
                                                                                                                                                                                                                                                                                                           cancer;
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Pred. No. 1.7e-88;
); Mismatches 0;
                                                                    Raitano
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                                                                                                                                                                                                                                                                                                          therapy;
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New composition comprising a substance that modulates the status of 121P1F1 or a molecule that is modulated by 121P1F1, useful for detecting,

WPI; 2004-060522/06

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RESULT 11
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ID ADM83
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AC ADM83
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CC composition comprising the novel composition in a human unit dose form, a CC recombinant protein comprising an antigen-binding region of a monoclonal CC antibody, a non-human transgenic animal that produces an antibody, a CC that immunospecifically binds to a 121PII-related protein (comprising CC that immunospecifically binds to a 121PII-related protein (comprising CC that immunospecifically binds to a 121PII-related protein (comprising CC that monoclonal antibody, a vector comprising a polymucleotide that encodes a single CC chain monoclonal antibody, a polymucleotide that encodes as an analogue CC peptide, delivering a Cytotoxic agent or a diagnostic agent to a cell that expresses 121PII, inhibiting growth of cancer cells that expresses 121PIII, inhibiting growth of cancer cells that expresses 121PIII, and the cells that composition, treating a manulaian immune response directed to 121PII, inducing an immune cresponse directed to 121PIII, inducing an immune cresponse directed of having cancer, monitoring 121PIII gene products in a biological sample from a patient who has or who is suspected of having cancer, monitoring the CC presence of cancer in an individual and an assay for detecting the CC presence of a 121PIII-related protein or polymucleotide in a biological composition may comprise a polymucleotide that comprises a 121PIII (ADM83793. The CC composition may comprise a polymucleotide that encodes at least one pelmide given in 16 Tables (given in the specification), the peptides composition is useful for detecting, treating or its composition and cancer, bladder cancer, kidney cancer, colon cancer, preferably prostate cancer, bladder cancer, kidney cancer to treat or prevent cancer that expresses or overexpresses concerned as a 121PIII protein (full-length or fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local :
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                                                       03-JUN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 206 AA;
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                                                                                                                                         ADM83835 standard; protein; 206 AA
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         gene 121P1F1 variant protein
                                                     (first entry)
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Pred. No. 1.4e-87;
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human leukocyte antigen; prostate cancer; bladder cancer; kidney colon cancer; lung cancer; pancreatic cancer; breast cancer; cervical cancer; stomach cancer; gene therapy; vaccine.
                                                                                                                                                             (CHAL/)
                                                                                                                                                                                                                       08-FEB-2001; 2001US-00779250.
                                                                                                                                                                                                                                                                                                         04-DEC-2003
Jakobovits A;
                       Challita-Eid PM, Hubert RS,
                                                                                                                                                                                                                                                               28-FEB-2002; 2002US-00087190.
                                                                                                      (AFAR/
                                                                                                                                              (RAIT/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cancer gene 121P1F1; cytostatic; cancer; chromosome 4q; HLA;
                                                                                                                                                               CHALLITA-BID P M.
HUBERT R S.
                                                              JAKOBOVITS
                                                                               AFAR DEH.
GEW.
                                                                                                                       FARIS M.
                                                                                                                                          RAITANO A B.
                       Raitano AB, Faris M,
                       Afar DEH,
                       Ge W;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cancer;
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New composition comprising a substance that modulates the status of 121PIFI or a molecule that is modulated by 121PIFI, useful for detecting, treating or preventing cancer e.g. prostate, bladder, colon, breast or lung cancer.

WPI; 2004-060522/06.

Example 5; SEQ ID NO 45; 211pp; English

Commodulates the status of 121PIF1 (a protein encoded by a cancer that modulates the status of 121PIF1 (a protein encoded by a cancer expressed composition comprising the novel composition included are a pharmaceutical composition comprising the novel composition in a human unit dose form, a crecombinant protein comprising an antigen-binding region of a monoclonal cantibody, a non-human transgenic animal that produce an antibody, a single chain monoclonal antibody in the treatment of the veriable domains of the heavy and light chains of a monoclonal antibody, a vector comprising a polynucleotide that encodes a single chain monoclonal antibody, a vector comprising a polynucleotide that encodes as analogue the variable domains of the heavy and light chains of a monoclonal contain monoclonal antibody, a polynucleotide that encodes a single chain monoclonal antibody, a vertoxic agent or a diagnostic agent to a cell chair expresses 121PIF1 (comprising administering to the cells the composition), treating a patient who bears cancer cells that express 121PIF1, inhibiting growth of cancer cells that expresses cancer response directed to 121PIF1, inducting an immune response directed to 121PIF1, inducting an immune comprises apolynucleotide that encodes at analogue presence of a 121PIF1 related protein or polynucleotide in a biological sample from a patient who has or who is suspected of having cancer. The composition may comprise a polynucleotide that encodes at least one composition encodes antiper one analogue related protein coding sequence provided that the coding sequence does cheing HLA (human leukocyte antigen)-binding epitopes from 121PIF1 or its generably prostate cancer, backeting, treating or treating cancer preferably prostate cancer, backeting, treating or concers of a cancer paracer that expresses or overexpresses concerned cancer. The composition is located on chronosome 4q. The present cancer cancer that expresses or overexpresses cancer is a 121PIF1 is located on chronosome 4q. The present cancer cance

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RESULT 12
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Best Local Similarity
The invention relates to a composition comprising a substance that modulates the status of 121P1F1 (a protein encoded by a cancer expressed gene) or a molecule that is modulated by 121P1F1 where status of the cell that expresses 121P1F1 is modulated. Also included are a pharmaceutical composition comprising the novel composition in a human unit dose form, a recombinant protein comprising an antigen-binding region of a monoclonal
                                                                                                                                                                                                                                                                                                                                                                                                                                                              human leukocyte antigen; prostate cancer; bladder cancer; kidney colon cancer; lung cancer; pancreatic cancer; breast cancer; cervical cancer; stomach cancer; gene therapy; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       03-JUN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADM83814 standard;
                                                                                                                      New composition comprising a substance that modulates the status of 121P1F1 or a molecule that is modulated by 121P1F1, useful for detecting, treating or preventing cancer e.g. prostate, bladder, colon, breast or
                                                                                                                                                                                                  Jakobovits A;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human cancer gene 121P1F1 protein fragment.
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                                                                                                                                                                                                                                                                                      (HUBE/)
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                                                                                      Example
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) RAITANO A B.
) FARIS M.
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GEW.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gene 121P1F1; cytostatic; cancer; chromosome 4q; HLA;
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Pred. No. 1.4
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RESULT 13
AAM40043
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XX AAM40
AC AAM40
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XX Alpha
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chain monoclonal antibody, a polynucleotide that encodes an analogue chair monoclonal antibody, a polynucleotide that encodes an analogue that expresses 121PIF1, inhibiting growth of cancer cells that expresses (212PIF1 (comprising administering to the cells the composition), treating a patient who bears cancer cells that express 121PIF1, generating a patient who bears cancer cells that express 121PIF1, generating a commandian immune response directed to 121PIF1, inducing an immune composition and individual and an assay for detecting the presence of a 121PIF1-related protein or polynucleotide in a biological sample from a patient who has or who is suspected of having cancer, monitoring the composition may comprise a polynucleotide that comprises a 121PIF1-cell related protein coding sequence provided that the coding sequence does not encode the entire amino acid sequence of 121PIF1 (ADM83793. The composition may comprises a polynucleotide that encodes at least one peptide given in 16 Tables (given in the specification), the peptides being HIA (human leukocyte antigen)-binding epitopes from 121PIF1 or its glice variants. The composition is useful for detecting, treating or preventing cancer, ladder cancer, kidney cancer, colon cancer, lung cancer, pancreatic cancer, breast cancer, corrient to prevent cancer. The composition can also be used as a 121PIF1. The gene for 121PIF1 is located on chromosome 4q. The present concer is a 121PIF1 protein (full-length or fragment).
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                                                                                                                    Human; nootropic; immunosuppressant; cytostatic; gene therapy; cance: peripheral nervous system; neuropathy; central nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
                                                                                                                                                                                                                                                                                                                                                 AAM40043
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                                                                                                                                                                                                                      Human polypeptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           antibody), a vector comprising a polynucleotide that encodes a single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          antibody, a non-human transgenic animal that produces an
                                                                                                 chemokinetic; thrombolytic;
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WO200153312-A1 Homo sapiens.

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RESULT 14
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21-JAN-2000;
25-APR-2000;
25-JUN-2000;
19-JUL-2000;
03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                          immunosuppressant and cytostatic activity. The polymucleotides are useful in gene therapy. A composition containing a polypeptide or polymucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system disease, such as Alzheimer's, Parkinson's disease, Huntington's disease, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and C.N.S disorders. Note: The sequence data for this patent did not form
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tang
Wang
                         ADD84547 standard; protein; 190 AA.
                                                                                                                                                                                                                                                                                                                                                          Sequence 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to human nucleic acids (AAI57798-AAI61369) encoded polypeptides (AAM38642-AAM42213) with nootropic,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26-JUL-2001.
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DB; AAI59199.
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Wang Z,
Goodrich
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2000US-00552317
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Zhang J,
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Best Local (
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Homo sapie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Composition comprising a substance that modulates the status of 121P1F1, useful in diagnosing, preventing, prognosticating or treating patients with cancer that expresses 121P1F1, such as breast, colon, ovarian or lung cancer.
                                                                                                                                                                                                                                                                                                 Sequence 190 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121P1F1; 121P1F1 modulation; human; chromosome 4q; cytostatic; gene therapy; vaccine; cancer; immune response; immunisation.
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GIPEDFDYID
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ilarity 100.0%;
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GIPEDFDYID

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RESULT 15
ADM83857
  The invention relates to a composition comprising a substance that comodulates the status of 121PIF1 (a protein encoded by a cancer expressed composition or a molecule that is modulated by 121PIF1 where status of the cell composition comprising the modulated. Also included are a pharmaceutical composition comprising the novel composition in a human unit dose form, a crecombinant protein comprising an antigen-binding region of a monoclonal antibody, a non-human transgenic animal that produces an antibody a chart immunospecifically binds to a 121PIF1-related protein (comprising the variable domains of the heavy and light chains of a monoclonal comprising the variable domains of the heavy and light chains of a monoclonal comprising antibody, a vector comprising a polynuclectide that encodes a single composition of comprising a polynuclectide that encodes an analogue peptide, delivering a cytotoxic agent or a diagnostic agent to a cell chain monoclonal antibody, a polynuclectide that encodes an analogue composition and comprising administering to the cells the composition), treating composition who bears cancer cells that express 121PIF1, generating a patient who has or who is suspected to 121PIF1, inducing an immune response directed to 121PIF1, inducing an immune composition may comprise a polynuclectide that comprises a 121PIF1 or sample from a patient who has or who is suspected of having cancer. The composition may comprise a polynuclectide that comprises a 121PIF1 The confidence of composition and comprises a polynuclectide that encodes at least one composition and comprises a polynuclectide that encodes at least one composition and comprises a polynuclectide that encodes at least one composition and comprises a polynuclectide that encodes at least one composition and comprises a polynuclectide that encodes at least one composition and comprises a polynuclectide that encodes at least one composition and composition in the specification of the peptides composition in the specification of the peptides compositi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human cancer gene 121P1F1 protein 16-205.
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(human leukocyte antigen)-binding
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121P1F1 or
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OM protein - protein search, using sw model

Run on: July 27, 2005, 09:28:34; Search time 40 Seconds (without alignments) 493.111 Million cell updates/sec

Title: Perfect score: US-10-087-190-3 1047

Sequence: MSKKKGLSAEEKRTRMMEIF.....FEENKIDRTFGIPEDFDYID 205

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters:

Minimum DB Maximum DB seq length: 0 seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 10

Listing first 45 summaries

Database

PIR\_79:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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284	1390	1298	400	284	168	168	284	879	629	308	1937	559	1938	559	285	284	199	764	284	880	2442	768	1356	1053	1281	174	128	210	Length
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S24348 T47237 B71603	TMRBA A39816 B27407 A25825 A60597	T19414 A64505 A22165 A34787	S19691 S00084 F84899
myosin heavy chain myosin II heavy ch RESA-H3 antigen PF	tropomyosin alpha tropomyosin 2, fib tropomyosin alpha tropomyosin alpha tropomyosin alpha tropomyosin 2, fib	hypothetical prote p115 homolog - Met tropomyosin alpha tropomyosin 1 alph	tropomyosin alpha, myosin heavy chain hypothetical prote

### ALIGNMENTS

hypothetical coiled-coil protein - fission yeast (Schizosaccharomyces pombe) C;Species: Schizosaccharomyces pombe C;Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 09-Jul-2004 C;Accession: T37610
R;Hunt, S:, Devlin, K:, Churcher, C:M.; Barrell, B.G.; Rajandream, M.A.; Walsh, submitted to the EMBL Data Library, September 1995
A;Reference number: Z21730
A;Accession: T37610

s.v.

A;Cross-references: UNIPROT:Q09739; EMBL:Z54096; PIDN:CAA90804.1; GSPDB:GN00066; SPDB:SPA;Experimental source: strain 972h-; cosmid cl3A11 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA A;Residues: 1-210 <HUN>

A;Gene: SPDB:SPAC13A11.03 Genetics:

A; Map position: A: Introns: 22/3

MVDCER	VDDG	KEVLQSL	NSMA'	KGIT	5 KGLSABEKRTRYMEIFSETKDVFQLKDLEKIAPKEKGITAMSVKEVLQSLVDDGMVDCER 64	OVFQLK	: E3	RMMEIFS!	ILSABEKRTI	5 -×	Qy	_
Gaps	6.	dels	In	76;	Matches 84; Conservative 36; Mismatches 76; Indels 6; Gaps	, Mis	36	ative	Conserva	84;	Matches	
		th 210;	Leng	2.	349; DB	Score		33.38	ni lavitu	tch tch	Query Match	
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123	122	63	65	44
123 QYTLELLHAKESELKLLKTQLSNLNHCNPETFELKNENTKKYMEAANLWTDQIHTLIAFC 182	122 RLAKELSSLRD-QREQLKAEVEKYKDCDPQVVEBIRQANKVAKBAANRWTDNIFAIKSWA 180	63 IGTSNYYWSFPSDAKRSRESVLGSLQAQLDDLKQKSKTLDENISFEKSKRDNEGTENDAN 122	65 IGTSNYYWAFPSKALHARKHKLEVLESQLSEGSQKHASLQKSIEKAKIGRCETE-ERT 121	4 KGLSLAEKRRRLEAIFHDSKDFFQLKEVEKLGSK-KQIVLQTVKDVLQSLVDDNIVKTEK 62
82	80	22	.21	Ñ

Ś 181 KRKFGFEENKIDRTFGIPEDFD 202

-RDMGADTNOIREYCSIPEDLD 203

밁

RESULT 2 T08972

A; Molecule type: DNA

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RESULT
JC5368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical protein YGL183c - yeast (Saccharomyces cerevisiae)

(;Alternate names: hypothetical protein G1604

C;Species: Saccharomyces cerevisiae

C;Date: 23-Feb-1996 #sequence revision 01-Mar-1996 #text_change 09-Jul-2004

C;Accession: S61134; S64200

C;Accession: S61134; S64200

R;Bertani, I.; Coglievina, M.; Zaccaria, P.; Klima, R.; Bruschi, C.V.

submitted to the EMBL Data Library, September 1995

A;Description: The sequence analysis of a 7.9 kb DNA fragment from the left ive new genes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Residues: 1-128 <BEV>
A;Cross-references: UNIPROT:Q9SZE5; EMBL:AL078470; GSPDB:GN00062; ATSP:F19B15.200
A;Experimental source: cultivar Columbia; BAC clone F19B15
C;Genetics:
C;Genetics:
A;Gene: ATSP:F19B15.200
A;Map position: 4
A;Introns: 13/3; 52/3; 88/3; 109/3
                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cros
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-174 <BER>
A;Residues: 1-174 <BER>
A;Cross-references: UNIPROT:P53102; EMBL:X91489; NID:g1143557; PIDN:CAA62791.1; PID:e199
A;Cross-references: UNIPROT:P53102; EMBL:X91489; NID:g1143557; PIDN:CAA62791.1; PID:e199
R;Bruschi, C.V.; Coglievina, M.; Bertani, I.; Klima, R.; Zaccaria, P.; Delneri, D.
R;Bruschi, C.V.; Coglievina, M.; Bertani, I.; Klima, R.; Zaccaria, P.; Delneri, D.
Submitted to the Protein Sequence Database, May 1996
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S61134
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A;Residues: 1-174 <BRU>
A;Cross-references: EMBL:Z72705; NID:g1322796; PIDN:CAA96895.1; PID:e243495; PID:g13227:
A;Experimental source: strain S288C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Reference number: S64183
A; Accession: S64200
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A; Accession: S61134
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49; Conserv
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                                                                                                                                                                                                                                                                                                      MSVKEVLQSLVD-DGMVDCERIGTSNYYWAFPSKALHARKHKLEVLESQLSEGSQKHASL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MMBIFSETKDVFQLKDLEKIAPKEKGITAMSVKEVLQSLVDDGMVDCERIGTSNYYWAFP
                                                                                 QENKQQIRLKKVHLEKTTDNIEILIDYLYKKFFLKPEQIRKEFGIPEEF
                                                                                                                          QANK----VAKEAANRWTDNIFAIKSWAKRKFGFEENKIDRTFGIPEDF 201
                                                                                                                                                                       KQELDKTLATGRRKKFTVGQKSYNREALLEKRKKIQDEIKK-KSNSLQKIESIRWDAAKI
                                                                                                                                                                                                                                                           MIVKDLVQQMIDEDGVISVEKCGNINIYWCFKNQTLQKLYDSSELIKKKIQEVKCDIATY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ---LRSVRQK---LESDLQGSNKRLAELVDQCEALKKGREESEERTEALTQLKDIEKKHK 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MLQIFYESQDFFLLKELEKWGPK-KGVISQSVKDVIQSLVDDDLVAKDKIGIS------
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                                                                                                                                                                                                                                                                                                                                              Score 168.5; DB Pred. No. 0.00021
2; Mismatches 6
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Pred. No. 2e-06;
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dynactin 1 - mouse
N;Alternate names: p150 Glued
N;Alternate names: p150 Glued
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 28-May-197 #sequence_revision 18-Jul-1997 #text_change 09-Jul-2004
C;Accession: JC5368
C;Accession: JC5368
R;Jang, W.; Weber, J.S.; Tokito, M.K.; Holzbaur, E.L.F.; Meisler, M.H.
Biochem. Biophys. Res. Commun. 231, 344-347, 1997
A;Title: Mouse p150Glued (dynactin 1) cDNA sequence and evaluation as a candidate for th A;Reference number: JC5368; MUID:97223454; PMID:9070275
A;Accession: JC5368
A;Molecule type: mtNA
A;Residues: 1-1281 cJAN>
A;Residues: 1-1281 cJAN>
A;Residues: 1-1281 cJAN>
A;Residues: This protein is a member of the oligomeric dynactin complex that is required
                                                                                                                                                                                                                                                                                                                                                                                                              A;Reference number: A41642; MUID:92098576;
A;Accession: A41642
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Species: Gallus gallus (chicken)
C;Date: 28-Aug-1992 #sequence_revision 28-Aug-1992 #text_change 09-Jul-2004
C;Accession: A41642
R;Gill, S.R.; Schroer, T.A.; Szilak, I.; Steuer, E.R.; Sheetz, M.P.; Cleveland, D.W.
J. Cell Biol. 115, 1639-1650, 1991
A;Title: Dynactin, a conserved, ubiquitously expressed component of an activator of
                                                                                                                                                                                                                                                                                                                                 A;Molecule type: mRNA
A;Residues: 1-1053 <GIL>
A;Cross-references: UNIPROT:P35458; GB:X62773; NID:g63920; PID:g63921
C;Keywords: cytoskeleton
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A; Map position:
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                                                                                                                                                               101 AKKEAKDALEAKERYMEEMADTADAIEMATLDKEMAEERAESLQQEVDSLKEKVEYLTMD
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                                                                                                                                                                                                                                                 53;
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                                                                                 LEILKHEIEEKGSDGAASSYQVKQLEEQNARLKEALVRMRDLSASEKQEHVKLQKQMEKK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LEILKAEIEEKGSDGAASSYQLKQLEEQNARLKDALVRMRDLSSSEKQEHVKLQKLMEK-
                                      KIGRCETEERTRLAKELSSIRDQREQIKAEVEK-YKDCD------PQVVEEIRQ 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LRETVGDLEAMNEMNDXLQENARETELELREQLD
                                                                                                                        GMV---DCERIGTSNYYWAFPSKALHARKHKLE---VLESQLSEG-SQKHASLQKSIEKA 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KNQELEVVRQQRERIQEELSQAESTIDELKEQVDAALGAE-EMVEMLTDRNLNLEEKVRE
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TELESLROOREKLOEEVKOAEKTVDELKEOVDAALGAEEMVETLTE
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                                                                                                                                                                                                                                                                       Score 130.5; Di
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  267
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RESULT 6
S32763
kinectin 1 -
                                                                                                hypothetical protein At2g39300 [imported] - Arabidopsis thaliana N;Alternate names: hypothetical protein T16B24.6 C;Species: Arabidopsis thaliana (mouse-ear cress) C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 05-Mar-1999 #sequence_revision 05-Mar-1999 #text_change 09-Jul-2004 C;Accession: T02572; F84915 R;Rounsley, S.D.; Kaul, S.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C submitted to the BMBI Data Library, August 1998 A;Description: Arabidopsis thaliana chromosome II BAC T16B24 genomic sequence. A;Reference number: Z14679 A;Accession: T02572 A;Status: translated from GB/EMBL/DDBJ A;Molecule type: DNA A;Residues: 1-768 <ROUN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Futterer, A.; Kruppa, G.; Kramer, B.; Lemke, H.; Kronke, M. Mol. Biol. Cell 6, 161-170, 1995
A;Title: Molecular cloning and characterization of human kinectin. A;Reference number: 137947; MUID:95306853; PMID:7787243
A;Accession: 137947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change
C;Accession: S32763; I37947
R;Kruppa, G; Fuetterer, A.; Lemke, H.; Kroenke, M.
submitted to the EMBL Data Library, April 1993
A;Description: Cloning and characterization of TAF, a novel tran A;Reference number: S32763
A;Accession: S32763
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A;Residues: 1-1356 <KRU>
A;Cross-references: UNIPROT:Q86UP2; EMBL:Z22551
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A; Residues: 1-1356 < RES>
A;Cross-references: UNIPROT:O80951; EMBL:AC004697; NID:g3402671; PID:g3402677
A;Experimental source: cultivar Columbia
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon,
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Pred. No. 2.3;
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A; Dialus. F-1
A;Molecule type: DNA
A;Residues: 1-768 <STO>
N-Cross-references: GB:AE002093; NID:g3402677; PIDN:AAC28980.1; GSPDB:GN00139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 centrosome associated protein CEP250 - human
C;Species: Homo sapiens (man)
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
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A; Introns: 80/2;
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                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: mRNA
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50; Conserv
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ALQQEQQQAQGQEERVKEKADALQGALEQAHMTLKERHGELQDH----KEQARR
                                 SLRDQREQLKAEVEKYKDCDPQVVEEIRQANKVAKEAANRWTDNIFAIKSWAKR
                                                                       ---SILLSQREQEIVVIQQQIQEAREQGELKEQSIQSQLDEAQRALAQRDQ-----ELE
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                                                                                                                                                                                                                                                                                         Score 116.5; I
Pred. No. 9.4;
47; Mismatches
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A;Reference number: A75001
A;Accession: F75103
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-880 - KRW>
A;Residues: 1-880 - KRW>
                                                                                                                                                                                                                                                                                                                                      C;Species: Sus scrofa domestica (domestic pig)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C;Accession: S24972
R;Mhitby, F.G.; Kent, H.M.; Stewart, F.; Stewart, M.; Xie, X.; Hatch, V.; Cc submitted to the EMBL Data Library, April 1992
A;Description: Structure of tropomyosin at 9 Angstroms resolution.
A;Reference number: S24972
A;Accession: 524972
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S24972
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                                                                                                                                                                                                                A;Cross-references: UNIPROT:P42639; EMBL:X66274; NID:g1926; PIDN:CAA46986.1; PID:g1927 C;Superfamily: tropomyosin C;Keywords: cardiac muscle; heart
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Gene: PAB0812
C;Superfamily: Archaeoglobus fulgidus conserved hypothetical protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      conserved hypothetical protein PAB0812 - Pyrococcus abyssi (strain Orsay)
C;Species: Pyrococcus abyssi
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C;Accession: F75103
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                                                                                                                                                                                                                                                                          A; Molecule type: mRNA
A; Residues: 1-284 <WHI>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Cross-references: UNIPROT: Q9UZC8; GB:AJ248286; GB:AL096836;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    submitted to the EMBL Data Library, July 1999
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                                                                                                                                                                                                                                                                                                                                  A; Accession: S24972
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local S
Matches 58
                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                Status: preliminary
                                                                                                                                                            Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             54 LVDDGMVDCERIGTSNYYWAFPSKAL-----HARKHKLEVLESQLSEGSQKHASL---
                        58
                                                              73
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                                                                                                                                        . Similarity 52; Conserv
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                                                            LAEKKATDAEADVASLNRRIQLFEEELDRAQ----ERLA-----TALQKLEEAEKAADE
                                                                                                  MSKKKGLSAE---EKRTRMMEIFSETKDVFQLKDLEKIAPKEKGITAMSVKEVLQSLVDD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VEELEDAKQVQKQIERLKARLKGLSPGEVIEKLESLEKERTEIEEAIKEITTRIGQMEQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         --DEYESKLRRLEKELSKWESELKAIEEVIKEGEKKKERAEEIREKLSEIEKRLEELKPY 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QREQLKA--EVEKYKDCDPQVVEEIRQANKVAKEAANRWTDNIFAIKSWAKRKFGFEENK 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        482
-GMVDCERIGTSNYYWAFPSKALHAR----KHKLEVLESQLSEGSQKH---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         38; Mismatches
                                                                                                                                      37;
                                                                                                                                                      Score 114; DB 2; Length 284; Pred. No. 1.3;
                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2;
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                                                                                                                                        61;
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                                                                                                                                      Gaps
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A; Reference number: $53896
A; Accession: $53899
A; Molecule type: DNA
A; Residues: 1-199 <POE>
A; Cross-references: EMBL: X86470; N.
R; Poehlmann, R.; Philippsen, P.
                                                                                                                                                                                                                                                                                                                                     tropomyosin TPM1 - yeast (Saccharomyces cerevisiae)
%,Alternate names: protein N2332; protein YNL079c
C;Species: Saccharomyces cerevisiae
C;Date: 08-Sep-1989 #sequence_revision 08-Sep-1989 #
C;Accession: A32183; S53899; S63011; S63018; S63928
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A32183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R; Bevan, M.; Weichselgartner, M.; submitted to the Protein Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical protein F10M6.170 - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #t. C;Accession: T05409
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T05409
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                                                                                                                                A;Cross-references: UNIPROT:P17536; R;Poehlmann, R.; Philippsen, P. submitted to the EMBL Data Library,
                                                                                                                                                                                            A;Accession: A32183
A;Molecule type: DNA
A;Residues: 1-199 <LIU>
                                                                                                                                                                                                                                                                                                   R;Liu, H.; Bretscher, A.
Cell 57, 233-242, 1989
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A; Note: F10M6.170
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                                                                                                                                                                                                                                                          A;Title: Disruption of the single tropomyosin gene in yeast results A;Reference number: A32183; MUID:89195234; PMID:2649250
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A;Experimental source: cultivar Columbia; BAC clone F10M6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-764 <BEV>
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A; Accession: T05409
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  42;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8 SAEEKRTRMMEIFSETKDVFQLKDLEKIAPKEK-----GITAMSVKEVLQSLV--DDG 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WAKR 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SQAREIEELKHKLRERDEERAALQSSLTLKEEELEKMRQ-----EIANRSKEVSMAISE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  40;
                              NID: g791101; PIDN: CAA60179.1;
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Pred. No. 3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -KVIESRAQKDEEKMEIQEIQLKEA--KHIAEDADRKYE
                                                                                                                                April 1995
                                                                                                                                                                           EMBL: M25501;
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                                                                                                                                                                           PIDN:AAA35174.1;
                              PID:g791105
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RESULT 13
JC6199
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A;Residues: 1-199 <POF>
A;Cross-references: EMBL:X86470; NID:g791101; PIDN:CAA60179.1; PID:g791105
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, April 1995
C;Genetics:
A;Molecule type: mRNA
A;Residues: 1-284 <LUQ>
A;Cross-references: UNIPROT:P87349; GB:U33450; NID:g1871357; PIDN:AAC60092.1; PID:g1871:C;Comment: This protein is a actin-binding protein.
C;Genetics:
C;Genetics: ATmS-1
A;Gene: ATmS-1
C;Kuperfamily: tropomyosin
C;Keywords: actin binding
                                                                                                                                                                                                     R;Luque, E.A.; Spinner, B.J.; Dube, S.; Dube, D.K.; Lemanski, L.F. Gene 185, 175-180, 1997
A;Title: Differential expression of a novel isoform of alpha-tropomyosin in A;Reference number: JC6198; MUID:97208870; PMID:9055812
A;Contents: skeltal muscle
A;Accession: JC6199
                                                                                                                                                                                                                                                                                                                                                       C;Species: Ambystoma mexicanum (axolot1)
C;Date: 11-Apr-1997 #sequence_revision 09-May-1997 #text_change 09-Jul-2004
C;Accession: JC6199
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Yeast 12, 391-402, 1996
A;Tille: Sequencing a cosmid clone of Saccharomyces cerevisiae chromosome A;Reference number: S63925; MUID:96267764; PMID:8701611
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A; Residues: 1-199 < POW>
A; Residues: 1-199 < POW>
A; Cross-references: EMBL: Z71355; NID:g1301970; PIDN: CAA95953.1; PID:g1301971; MIPS:YNL07
A; Experimental source: strain S288C
A; Experimental source: strain S288C
R; Soler-Mira, A.; Saiz, J.E.; Ballesta, J.P.G.; Remacha, M.
submitted to the Protection Sequence Database, April 1996
                                                                                                                                                                                                                                                                                                                                                                                                           alpha-tropomyosin S-1 - axolotl
C;Species: Ambystoma mexicanum
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C; Superfamily: tropomyosin TPM1
C; Keywords: coiled coil; cytosk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Gene: SGD:TPM1
A;Cross-reference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              submitted to the Protein A; Reference number: S6299 A; Accession: S63011 A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  밁
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A; Accession: S63018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: EMBL:Z71355; NID:g1301970; PIDN:CAA95953.1; PID:g1301971; A;Experimental source: strain S288C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type:
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Best Local S
Matches 46
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    148 DPQVVE 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  186 KKELDE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 46;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DCERIGTSNYYWAFPSKALHARKHKL----EVLESQLSEG------SQK 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LEAESWOEKYEELKEKNKDLEQ-ENVE----KENQIKSLTVKN--QQLEDEIEKLEAGLS 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DSKQTEQDNVEKENQIKSLTVKNHQLEEEIEKLEAELAESKQLSEDSHHLQSNNDNFSKK 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA
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S62997
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24.7%; Pred. No. 1;
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A;Molecule type: DNA
A;Residues: 1-285 <CLA>
A;Residues: 1-285 <CLA>
R;Reinach, F.C.; MacLeod, A.R.
R;Reinach, F.C.; MacLeod, T.R.
Nature 322, 648-650, 1986
A;Title: Tissue-specific expression of the A;Reference number: A24199; MUID:86311274;
A;Accession: A24199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Title: Organization of the hTM(nm) gene. A;Reference number: S02554; MUID:88332987; A;Accession: S06210
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R;Clayton, L.; Reinach, F.C.; Chumbley, G.M.; MacLeod, A.R. J. Mol. Biol. 201, 507-515, 1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Species: Homo sapiens (man)
C;Date: 02-Jun-1988 #sequence_revision 02-Jun-1988 #text_change 13-Aug-1999
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                                                                                                                                                                                                                                                                                                                                                                                                           C; Keywords: alternative splicing; coiled coil; muscle; skeletal muscle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Residues: 1-285 < REI >
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Status: not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C; Accession: S06210; A24199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tropomyosin NM, skeletal muscle - human
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Best Local Similarity
Matches 48; Conserv
                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                               Match 10.7%;
Local Similarity 23.5%;
                                                                             178
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                                                                                                                                                                                                                                                                                 1 MSKKKGLSAEEK---RTRMMEIFSETKDVFQ-----LKDLEKIAPK-EKGITAMSV 47
                                                                                                                                                                                                                                                                                                                              52;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QKSIEKAKI--GRCETEERTRLAKELSSLRDQREQLKAEVEKYKDCDPQVVEEIRQANKV 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R----ALKDEEKMELQEI------QLQEAKHIAEEADRKYEEVARKLVIIEGDL 176
                                  KVAKEAANRWIDNIFAIKSWAKRKFGFEENKIDRIFGIPED 200
                                                                                                                 EKAKIGRCETEERTRIA-----KELSSLRDQREQLKAEVEKYKDCDPQVVEEIRQAN 159
                                                                                                                                                        R----ALKDEEKMELQEI-------QLKEAKHIAEEADRKYEEVARKLVIIEGDL
                                                                                                                                                                                                 KEVLQSLVDDGMVDCERIGTSNYYWAFPSKALHARKHKLEVLESQLSEGSQKHASLQKSI 107
                                                                                                                                                                                                                                            LAEKKAADAEAEVASLNRRIQLVEEELDRAQERLATALQKLEEAEKAADESERGMKVIEN 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AKEAANRWIDNIFAIKSWAKRKFGFEENKID 192
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KEVLQSLVDDGMVDCERIGTSNYYWAFPSKALHARKHKLEVLESQLSEGSQK----HASL 103
                                                                                                                                                                                                                                                                                                                              Conservative
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                                                                           ----AEFAERTVAKLEKSID 254
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                                                                                                                                                                                                                                                                                                                            41;
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1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                  Score 112; DB 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             human tropomyosin
PMID:3018581
KLEKTIDDLED
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RESULT 15 S49143

EG10 protein - tapeworm C; Species: Echinococcus

(Echinococcus granulosus

granulosus)

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C;Date: 16-Feb-1995 #sequence_revision 12-May-1995 #text_change 15-Mar-2004
C;Accession: S49143
R;Frosch, P.M.; Hartmann, M.; Sygulla, L.; Margutti, P.; Frosch, M.
submitted to the EMBL Data Library, January 1994
A;Description: Identification of a cDNA clone from the larval stage of Echinococcus gran A;Reference number: S49143
A;Accession: S49143
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-559 <FRO>
A;Cross-references: EMBL:Z29489; NID:g509759; PIDN:CAA82625.1; PID:g509760
C;Superfamily: ezrin/radixin/moesin; protein 4.1 membrane-binding domain homology
F;12-293/Domain: protein 4.1 membrane-binding domain homology <B41>
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Search completed: July 27, 2005, 09:41:43
Job time : 42 secs
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Best Local Similarity
Matches 49; Conserv
                                                                                           395
                                                                                                                                                                            348 EKE-----SDLADMKNKASAYESKIAELEMILQQERHARESLQKSQDKLAEM 394
                                                                                                                                                                                                                                                                          113 GRCETEERTRLAKELSSLRDOREOLKAEVEKYKDCDPOVVEEIROANKVAKEAANR 168
                                                                                                                                                                                                                    NRKLKEETAASAEERNRLMAQRDEVQREVEAQK-----VAMAKKEAEKAQAEAELR 445
                                                                                                                                                                                                                                                                                                                                                                          10.7%; Score 112; DB 2; Length 559; ilarity 27.8%; Pred. No. 3.7; Conservative 34; Mismatches 61; Indels
                                                                                                                                                                                                                                                                                                                                                                               32;
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Title:
Perfect score:
Sequence:
                                                                                 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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                                              Database :
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Gapop 10.0 , Gapext 0.5
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UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*
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1047
1 MSKKKGLSAEEKRTRMMEIF......FEENKIDRTFGIPEDFDYID 205
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Result

Result		Query		3	COMPANYABLE	•
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ω	948	90.5	205	N	Q9D0A1	,_
4	644	•	220	N	Q6DC61	Q6dc61 brachydanio
ហ	462	44.1	196	N	Q86EZ8	~
6	440	42.0	230	N	Q8GYD2	arabid
7	427	•	207	N	Q6H432	
8	349	•	210	ب	YA53_SCHPO	) schize
9	340.5	32.5	203	N	Q8SUĀ9	9
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11	0	•	203	N	Q7QTX0	
12	332.5	٠	179	N	646090	w
13	N	•	196		Q7RH53	
14	266.5	25.5	211		Q6BQL5	U
15		21.1	225		Q75CH5	
16	206.5	•	225		Q6CSX5	
17	197	18.8	128		Q9SZE5	v
18	175	•	222		Q6FL56	01
19	168.5	•	174		YGT3_YEAST	N
20	153.5	14.7	101		Q6E679	
21	•	٠	910		Q7T2F8	Q7t2f8 brachydanio
22	•	•	1281		DYNA_MOUSE	mus r
23	•	•	890		Q6AWB1	homo
24	4	•	890		Q6AWB3	homo
25	134.5	•	1139		Q6IQ37	homo
26		12.8	1264	N	Q6NZM3	mus r
27		•	1278	ب	DYNA_HUMAN	Q14203 homo sapien
28	•	•	1278	N	Q6MZZ3	homo
29	131.5	•	1280	ب	DYNA_RAT	3 rattus
30	•	•	1224	Н	DYNA CHICK	P35458 gallus gall
31	•	12.1	1232	N	Q6PCJ1	xenopu

45	44	43	42	41	40	39	38	37	36	35	34	33	32
118.5	120	120	120.5	120.5	120.5	121.5	121.5	121.5	122	122	122	122.5	126
11.3	11.5	11.5	11.5	11.5	11.5	11.6	11.6	11.6	11.7	11.7	11.7	11.7	12.0
1177	1120	882	1732	448	172	1364	1357	995	18534	18519	10578	797	609
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Q877 <u>1</u> 1	ERC1_MOUSE	RASO PYRFU	Q9VJ35	Q84H59	Q824V3	KTN1_CHICK	KTN1_HUMAN	Q6F1N4	Q8ISF7	Q8ISF6	Q8ISF5	Q6GLB3	Q8TXA4
•	•	•	Q9vj35 dz	Q84h59 an	Q824v3 ch	Q90631 ga	Q86up2 hc	Q6fln4 me	_	•	•		Q8txa4 me
pyrococcus	mus musculu	/rococcus	drosophila	naplasma m	lamydophi	. gallus gall	omo sapien	mesoplasma	caenorhabdi	caenorhabdi	caenorhabdi	xenopus tro	methanopyru

# ALIGNMENTS

RESULT 1

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Query Match	SEQUENCE FROM SEQUENCE FROM TISSUE-Lymph; Strausberg R.; Strausberg R.; Submitted (JUN EMBL; AY028916 EMBL; BC032142 InterPro; IPR0 InterPro; IPR0 Pfam; PF03962; SEQUENCE 205	Whiting M., Madan Blakesley R.W., T Rodriguez A.C., G Krzywinski M.I., Jones S.J., Marra "Generation and i and mouse cDNA se Proc. Natl. Acad.	Stapleton M Brownstein I Raha S.S., Bosak S.A., Richards S. Villalon D.I Fahey J., H	SEQUENCE FROM TISSUE-Lymph, MEDLINE-223882 Strausberg R.L Klausner R.D., Altschul S.F., Hopkins R.F., Diatchenko L.,	Name=GAJ; Name=GAJ; Homo sapiens (Human Eukaryota; Metazoa; Mammalia; Eutheria; NCBI_TaxID=9606; [1] SEQUENCE FROM N.A. SOUIS G., Hofer H.W Submitted (MAR-2001)	776 Q9BWT6 Q9BWT6; Q9BWT6; 01-JUN-2001 01-JUN-2001 25-OCT-2004
10	; ; N-2002) 6; AAK26 2; AAH32 005647; 009058; ; Mnd1; 5 AA; 2	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffar Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., But Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Jones S.J., Marra M.A.; Jones S.J., Marra M.A.; "Generation and initial analysis of more than 15,000 ful and mouse cDNA sequences."; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E. Brownstein M.J., Uddin T.B., Toshiyuki S., Carninci R., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Anaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W. Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Cibbs R.A., Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Cibbs R.A., Fahey J., Helton B., Ketteman M., Madan A., Rodrigues S., Sanchez A.	[2] SEQUENCE FROM N.A. TISSUB=Lymph; TISSUB=Lymph; MEDLINE=23388257; PubMed=12477932; DOI=10.1073/pnas.242603899 MEDLINE=23388257; PubMed=12477932; DOI=10.1073/pnas.242603899 Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Sthulars R.F., Collins F.S., Wagner L., Schammen C.M., Schuldranklausberg R.D., Collins F.S., Wagner L., Schaefer C.F., Bhar Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhar Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hareh Flopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hareh Flopkins R.F., Jordan H., Moore T., Max R.D., Rubin G.M., Horg L., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Horg L.,	∪. <sup>-</sup>	PRELIMINARY (TrEMBLrel. (TrEMBLrel. (TrEMBLrel.
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DB 2;		Shevchenko Y., Bou Ween E.D., Dickson M utz J., Wyers R.M., lus D.E., Schnerch of more than 15,000 16899-16903(2002).	Casavant T.L., Casavant T.L., Carninci P., Abramson R.D., Ialek J.A., Fun A.M., Gay L.J Lu X., Cibbs Lu X., Cibbs	1073/pnas.2 H., Derge J. Thenmen C.M., Schaefer C.F. I., Wang J., Rubin G.M.,		r; 205 AA. :ed) sequence update) annotation update)
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K. MEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

K. MEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

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Barrywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
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Mammalia; Eutheria; Rodentia;
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MGD; MGI:1924165; 2610034E18Rik.
InterPro; IPR005647; Mndl.
Pfam; PF03962; Mndl; 1
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Q9DOA1;
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01-JUN-2001
01-JUN-2001
01-MAR-2004
SEQUENCE FROM N.A.

STRAIN=C57BL/6J; TISSUE=Whole body;

MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;

MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;

Shibata K., Itoh M., Alzawa K., Nagaoka S., Sasaki N., Carninci P.,

Konno H., Akiyama J., Nishi K., Kiteunai T., Tashiro H., Itoh M.,

Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,

Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,

Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,

Pujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,

Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,

Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;

Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;

RIKEN integrated sequence analysis (RISA) system-384-format
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
101-JUN-2001 (TrEMBLrel. 26, Last annotation update)
101-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Mus musculus 10 days embryo whole body cDNA, RIKEN full
enriched library, clone:2610034E18 product:GAJ homolog.
                                                                                                                                                                                                                                                                                                                                          STRAIN=C57BL/6J; TISSUE=Whole body;
MEDLINE=2049374; PubMed=11042159; DOI=10.1101/gr.145100;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K.,
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
"Normalization and subtraction of cap-trapper-selected cDNAs prepare full-length cDNA libraries for rapid discovery of new Genome Res. 10:1617-1630(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The FANTOM Consortium, the RIKEN Genome Exploration Research Group "Analysis of the mouse transcriptome based c 60,770 full-length cDNAs.";
Nature 420:563-573(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Whole body;
MEDLINE=21085660; PubMed=11217851;
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STRAIN=C57BL/6J; TISSUE=Whole body;
MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. STRAIN=C57BL/6J; T
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STRAIN=C57BL/6J; TISSUE=Whole
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RIKEN FANTOM Consortium,
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"High-efficiency full-length cDNA cloning.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mammalia;
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Rodentia;
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Sciurognathi; Muridae
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; Murinae: Mds.
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Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
RA Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
RA Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
RA Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
RA Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
Muramatsu M., Hayashizaki Y.,
L Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
R MGD; MGI:1924166. 26100275.1; ...
R MGD; MGI:1924166. 26100275.1; ...
        RANGE 
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SEQUENCE FROM N.A.

C. STRAIN-Singapore local strain; TISSUB-Embryo;

C. STRAIN-Singapore local strain; TISSUB-Embryo;

X. Pubmed-12477932; DOI=10.1073/pnas.242603899;

X. Strausberg R.L., Felingold E.A., Grouse L.H., Derge J.G.,

X. Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

X. Klausner R.D., Collins F.S., Buetow K.H., Schaefer C.F., Bhat N.K.,

X. Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

X. Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

X. Hopkins R.F., Jordan H., Moore T., A., Rubin G.M., Hong L.,

X. Hopkins R.F., Jordan H., Moore T., Casavant T.L., Scheetz T.E.,

X. Hopkins R.F., Jordan R.J., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

X. Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

X. Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

X. Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

X. Raha S.S., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

X. Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

X. Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
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Best Local S
Matches 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Brachydanio rerio (Zebrafish)
Eukaryota; Metazoa; Chordata;
Actinopterygii, Neopterygii; T
Cyprinidae; Danio
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Pfam; PF03962; Mnd1; 1.
SEQUENCE 205 AA; 23909
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. 10:1757-1771(2000).
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Ostariophysi; Cypriniform
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MEDILINE=22879925; PubMed=12973349; DOI=10.1038/ng1236;
Hu W., Yan Q., Shen D.K., Liu F., Zhu Z.D., Song H.D., Xu X.R.,
Wang Z.J., Rong Y.P., Zeng L.C., Wu J., Zhang X., Wang J.J., Xu X.N.,
Wang S.Y., Fu G., Zhang X.L., Wang Z.Q., Brindley P.J., McManus D.P.,
Xue C.L., Feng Z., Chen Z., Han Z.G.;
"Evolutionary and biomedical implications of a Schistosoma japonicum
complementary DNA resource.";
Nat. Genet. 35:139-147(2003).
EMBL; AY223066; AAP060891; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-Singapore local strain; TISSUE-Embryo; Director MGC Project; Submitted (JUL-2004) to the EMBL/GenBank/DDBJ EMBL; BC07823; AAH78223.1; -. InterPro; IPR005647; Mndl. InterPro; IPR00968; Wing_hlx_DNA_bnd. Pfam; Pf03962; Mndl; 1. SEQUENCE 220 AA; 25176 MW; 90DEAA69311F4B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Schistosoma japonicum (Blood fluke).
Eukaryota; Metazoa; Platyhelminthes;
Schistosomatoidea; Schistosomatidae;
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01-JUN-2003 (TrEMBLrel. 24,
01-OCT-2003 (TrEMBLrel. 25,
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                                                                                                                                                                                                                                                   InterPro; IPR005647; Mnd1.
Pfam; PF03962; Mnd1; 1.
SEQUENCE 196 AA; 23163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Clone ZZD1259 mRNA sequence.
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                                                                                                                                                Score 462; DB 2;
Pred. No. 1.2e-20;
4; Mismatches 68
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G.G.,
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Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; teudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
Seki M., Iida K., Satou M., Sakurai T., Akiyama K., Ishida Nakajima M., Enju A., Kamiya A., Narusaka M., Carninci P., Hayashizaki Y., Shinozaki K., Shinozaki K., Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.
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Q8GYD2;
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EMBL; AK117713; BAC42364.1; -.
EMBL; BT005435; AA063855.1; -.
InterPro; IPR005639; endotoxin_N.
InterPro; IPR005647; Mndl.
Pfam; PF03962; Mndl; 1.
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01-MAR-2003 (TrEMBLrel.
05-JUL-2004 (TrEMBLrel.
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SNNFPQAKEQLEHLYTEAGITEDFDYIE
                                                   KRKFGFEENKIDRTF---
                                                                                                                                                              TRLAKELSSLRDQREQLKAEVEKYKDCDPQVVEEIRQANKVAKEAANRWTDNIFAIKSWA
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230 AA; 2
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el. 23, Last sequence update)
el. 27, Last annotation update)
at4g29170/F19B15_200 (Hypothet
                                                                                                                                                                                                                                                                                                                                                                                                                                                43;
                                                   -GIPEDFDYID 205
                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 440; DB 2; I
Pred. No. 3.2e-19;
3; Mismatches 70;
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YA53_SCHPO

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01-NOV-1995 (Rel. 32, Created)

01-NOV-1995 (Rel. 32, Last sequence up

05-JUL-2004 (Rel. 44, Last annotation

Hypothetical protein C13A11.03 in chro

ORFNames=SPAC13A11.03;
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Q6H432;
05-JUL-2004
05-JUL-2004
05-JUL-2004
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MEDIINE-21848401; PubMed=11859360; DOI=10.1038/nature724; Wood V., Gwilliam R., Rajandream M.A., Lyne R., Lyne R., Stewart A., Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S., Erooks K., Brown D., Brown S., Chillingworth T., Churcher C.M., Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A., Gentles S., Goble A., Hamiln N., Harris D., Hidalgo J., Hodgson G., Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K., James K., Jones L., Jones M., Leather S., McDonald S., McLean J., Monopy P., Moule S., Mungall K., Murphy L., Niblett D., Odell C., Oliver K., O'Neil S., Pearson D., Quail M.A., Rabbinowitsch E., Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
                                                                                                                                                                                                                                        Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
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; Pred. No. 1.7e-18;
44; Mismatches 71
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A Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
A Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
A Woodward J., Vonstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
A Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
A Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
A Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
A Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
A Golibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
A Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
A Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
A Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
A Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
Crutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
A Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.,
"The genome sequence of Schizosaccharomyces pombe.";

Nature 415:871-880(2002).
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Matches 84
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01-JUN-2002
01-JUN-2002
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein ECU10_1600.
Name=ECU10_1600;
Encephalitozoon cuniculi GB-M1.
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InterPro; IPR009058; Wing_hlx_DNA_bnd
Pfam; PF03962; Mnd1; 1.
      MEDLINE=21576510; PubMed=11719806; DOI=10.1038/35106579;
Katinka M.D., Duprat S., Cornillot E., Metenier G., Thom
Prensier G., Barbe V., Peyretaillade E., Brottier P., Wi
                                                                                                                                                                                         Eukaryota; Fungi; Microsporidia; Unikaryonidae; Encephalitozoon.
NCBI_TaxID=284813;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q8SUA9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hypothetical SEQUENCE 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GeneDB_SPombe; SPAC13A11.03; -.
                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        T37610; T37610
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KRKFGFEENKIDRTFGIPEDFD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IGTSNYYWAFPSKALHARKHKLEVLESQLSEGSQKHASLQKSI--EKAKIGRCETE-ERT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -RDMGADTNQIREYCSIPEDLD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24224 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 349; DB 1
Pred. No. 9e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  F4A546F070A37665 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1; Length 210;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               76;
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                                   Thomarat
            Wincker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Whitehead S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gh a collaboration EMBL outstation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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RESULT 10
Q6WDA3
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                                                                                  Query Match
Best Local S
Matches 70
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Best Local
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                                                                                                                                                                                                                                                                                Q6WDA3;
05-JUL-2004
05-JUL-2004
                                                                                                                                             Ramesh M.A., Malik S.B., Logsdon J.M.
Submitted (ARR-2003) to the EMBL/GenBa
EMBL, AY295092; AAQ24512.1; -
InterPro; IPR005647; Mnd1.
InterPro; IPR009589; Wing_hlx_DNA_bnd.
Efgr. PRO?
                                                                                                                                                                                                                                                             Mndl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (APR-2001) to the EMBL; AL590449; CAD25881.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Genome sequence and gene compaction Encephalitozoon cuniculi.";
                                                                                                                                                                                                                         Eukaryota; Diplomonadida; Hexamitidae; Giardiinae; Giardia.
NCBI_TaxID=5741;
                                                                                                                                                                                                                                                                                                                   Q6WDA3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hypothetical
SEQUENCE 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR002114; HPT SerP.S.
InterPro; IPR005647; Mndl.
InterPro; IPR009568; Wing hlx DNA bnd.
Pfam; PF03962; Mndl; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genoscope;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-GB-M1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                 Giardia lamblia (Giardia intestinalis).
                                                                                                                                                                                                                                                                        05-JUL-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS00589; PTS_HPR_SER; UNKNOWN_1.
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                                                                                                                           PF03962; Mnd1;
NCE 203 AA; 7
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                                                                                               Similarity
             IGTSNYYWAFPSKALHARKHKLEVLESQLSEGSQKHASLQKSIEKAKIGRCETEERTRLA
                                                                                                                                                                                                                                                                                                                                                                      KFGFEENKIDRTFGIPEDFDYI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LSABEKRTRMMEIFSETKDVFQLKDLEKIAPKEKGITAMSVKEVLQSLVDDGMVDCERIG
                                                      KGLSAEEKRTRMMEIFSETKDVFQLKDLEKIAPKEKGITAMSVKEVLQSLVDDGMVDCER
                                                                                                                                                                                                                                                                                                                                                                                                                 LNALMKIEQDORE----ELGKFEETDPIAYDKLVADRKEMADECNRIIDNVFIIQDYICS
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                                         KGTSLDEKKERLLEEMLKRGEIYSNKTIETLS-KPTGISSMVIKAVLQALVNEDLVDTDK
                                                                                                                                                                                                                                                                                                                                                                                                                                      LSSL----RDOREOLKAEVEKYKDCDPQVVEEIRQANKVAKEAANRWTDNIFAIKSWAKR
IGASTYYWCFASKRSQAARTELARLQKALEEQTNFIDKATARIEELKVGREETEERSSLL
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                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
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                                                                                                                             23278 MW; CC0625DCDC4158C0 CRC64;
                                                                                             32.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             32.5%;
                                                                                                                                                                                                                                                                      27,
                                                                                                                                                                                  Logsdon J.M. Jr.;
the EMBL/GenBank/DDBJ
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                                                                                   46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL/GenBank/DDBJ
                                                                                  Last
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                                                                                                                                                                                                                                                                                             Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 340.5; DB
Pred. No. 2.8e-13
0; Mismatches 7
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                                                                                                                                                                                                                                                                                                                                                                                            204
                                                                                                                                                                                                                                                                                  sequence update)
                                                                                                                                                                                                                                                                        annotation
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                                                                                               .8e-13;
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                                                                                                         DB
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  122
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RESULT 11
Q7QTX0
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Q6Q9F9
       RRR RR OCC OCC DIT DIC
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Best Local S
Matches 70
                                                                                                                                                                                                                   05-JUL-2004
05-JUL-2004
05-JUL-2004
                                                                                        MND1 domain containing protein.
Aedes aegypti (Yellowfever mosquito).
Bukaryota; Metazoa; Arthropoda; Hexapo
Neoptera; Endopterygota; Diptera; Nem.
NCBI_TaxID=7159;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAR-2004 (TrEMBLrel. 26,
01-MAR-2004 (TrEMBLrel. 26,
01-MAR-2004 (TrEMBLrel. 26,
SEQUENCE FROM N.A.
TISSUE=Salivary gland;
Chandra P.K., Wikel S.K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Draft sequence of the Giardia lamblia genome.";
Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GLP_76_12374_11763.
Giardia lamblia ATCC 50803.
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                                                                                                                                                                                                                                                                                              Q6Q9F9;
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                                                                                                                                                                                                                                                                                                                   Q6Q9F9
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InterPro; IPR009058; Wing_hlx_DNA_bnd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Morrison H.G., McArthur A.G., Adam R.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=WB C6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          preliminary data.
L; AACB01000100; EAA38463.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                              183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           185
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GFEENKIDRTFGIPEDFDYID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KEKLALQVKLEEQRGTFRDLLKNDPDVAQKLRNYTDIAKQEANLWTDNIFCLQKYMLTKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IGTSNYYWAFPSKALHARKHKLEVLESQLSEGSQKHASLQKSIEKAKIGRCETEERTRLA 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KGLSAEEKRTRMMEIFSETKDVFQLKDLEKIAPKEKGITAMSVKEVLQSLVDDGMVDCER
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                                                                                                                                                                                                                                                                                                                                                                                                                                              QMDKKTVSTALGITGEFDYLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KELSSLRDQREQLKAEVEKYKDCDPQVVEEIRQANKVAKEAANRWTDNIFAIKSWAKRKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IGASTYYWCFASKRSQAARTELARLQKALEEQTNFIDKATARIEELKVGREETEERSSLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KGTSLDEKKERLLEEMLKRGEIYSNKTIETLS-KPTGISSMVIKNVLQALVNEDLVDTDK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  203 AA;
                                                                                                                                                                                                                (TrEMBLrel. 27, Created)
(TrEMBLrel. 27, Last sequence update)
(TrEMBLrel. 27, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23278 MW; CC0625DCDC4158C0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       32.5%;
                                                                                                                      Diptera; Nematocera; Culicoidea; Aedes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hexamitidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  46; Mismatches
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Last annotation updat
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Pred. No. 2.0
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                                                                                                                                          Hexapoda; Insecta; Pterygota;
                                                                                                                                                                                                                                                                                                                     179
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RESULT 13
Q7RH53
ID Q7RH5
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Best Local S
Matches 66
                                                                                                                                               Matches
                                                                                                                                                             Query Match
Best Local :
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O7RH53;
O1-MAR-2004 (TrEMBLrel. 2
O1-MAR-2004 (TrEMBLrel. 2
O1-MAR-2004 (TrEMBLrel. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted
EMBL; AY55
                                                                                                                                                                                                                                                                                                                                                               PubMed=1236865; DOI=10.1038/nature01099;
Carlton J.M., Angiuoli S.V., Suh B.B., Kooi T.W., Pertea M.,
Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,
Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,
Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,
Shallom S.J., van Aken S.E., Riedmuller S.B., Feldblyum T.V.,
Cho J.K., Quackenbush J., Sedegah M., Shoaibi A., Cummings L.M.,
Plorens L., Yates F.R. III, Raine J.D., Sinden R.E., Harris M.A.,
Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B.,
van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,
Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.
                                                                                                                                                                                                                                                                                                         "Genome sequence and comparative analysis of the model parasite Plasmodium yoelii yoelii."; Nature 419:512-519(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Plasmodium yoelii yoelii.
Bukaryota; Alveolata; Api
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR005647; Mnd1.
Pfam; PF03962; Mnd1; 1.
SEQUENCE 179 AA; 20900 MW;
                                                                                                                                                                                                                                 preliminary data.
EMBL; AABLO1001237; EAA15959.1;
InterPro; IPR005647; Mnd1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Name=PY04140;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens GAJ, putative
                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                         Carucci D.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=73239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                               CAUTION: The sequence shown here is derived EMBL/GenBank/DDBJ whole genome shotgun (WGS)
                                                                                                                                                                                                                                                                              EMBL/GenBank/DDBJ whole genome shotgun
 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121
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                             61
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                                                                                                                                                                                                                       PF03962;
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                                                                                                                                                             Similarity
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 ETEERTRLAKELSSLRDQREQLKAEVEKYKDCDPQVVEEIRQANKVAKEAANRWTDNIFA 175
                                                                                                          KKKGLSABEKRTRMMBIFSETKDVFQLKDLEKIAPKEKGITAMSVKEVLQSLVDDGMVDC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SSEMFEKLNTLKEKQKQLSSKLDKAKLKQSDQNSVDKMNRNLPDLHDAANRWDGTTYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MSK-KKGLSAEEKRTRMMEIFSETKDVFQLKDLEKIAPKEKGITAMSVKEVLQSLVDDGM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RTRLAKELSSLRDQREQLKAEVE--KYKDCDPQVVEEIRQANKVAKEAANRWTDNIFA 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VETDKIGSSQYYWFFPAKKRKLKQQVFEQLKQEMEQSNDKIAELQKRIGTIKESQGESSR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VDCERIGTSNYYWAFPSKALHARKHKLEVLESQLSEGSQKHASLQKSIEKAKIGRCETEE 119
                             EKVGSQNVFWILKTEESSILQNKYQELKDKKEEYEEMAQAEKENYAELENSLS-----L
                                                      ERIGTSNYYWAFPSKALHARKHKLEVLESQLSE-----GSQKHASLQKSIEKAKIGRC
                                                                                     KKKGKSNEDKKLILYDIMLESESFFILKELEALAPK-KGIRSIFVKDLIQQLIDDNKIKS
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                                                                                                                                                                                                       962; Mnd1;
196 AA; 2
                                                                                                                                               Conservative
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                                                                                                                                                                                                         23066 MW;
                                                                                                                                                          26.5%;
29.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                52;
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Last annotation updat
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                                                                                                                                                             Score 277;
Pred. No. 1.
                                                                                                                                                                                                       7FD8820707329074 CRC64;
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                                                                                                                                      DB 2,
1.9e-09;
76;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 179;
                                                                                                                                               Indels
                                                                                                                                                                            196;
                                                                                                                                                                                                                                                                                                                                        rodent malaria
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                                                                                                                                             14;
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                                                                                                                                             Gaps
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RESULT 14
Q6BQL5
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Best Local S
Matches 61
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Q6BQL5;
25-OCT-2004
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Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talla E.,
Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A.,
Barbe V.,
Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C.,
Boisrame A., Boyer J., Cattolico L., Confanioleri F., de Daruvar A.,
Despons L., Fabre E., Faithead C., Ferry-Dunazet H., Groppi A.,
Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
Nicaud J.M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,
Pellenz S., Potier S., Richard G.F., Strub M.L., Suleau A.,
Swennene D., Tekaia F., Wesolowski-Louvel M., Westhof E., Wirth B.,
Zeniou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,
Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,
Wincker P. Schrift II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (JUL-2004) to the EMBL; CR382137; CAG87731.1; InterPro; IPR005647; Mnd1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORFNames=DEHA0E04994g;
Debaryomyces hansenii (BS767.
Bukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Debaryomyces.
NCBI_TaxID=284592;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF03962; Mnd1;
NON_TER 1
SEQUENCE 211 AA; 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bouchier C., Caudron B., Scarp Wincker P., Souciet J.L.; "Genome evolution in yeasts.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=CBS767;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Similar to CA3413 | IPF9239 Candida albicans IPF9239 unknown function
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nature
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                                                                                                                                                                                                                                                                                                                                                       KCGTTNLYWCF------KFDKIKTLQTQYNNYQNKLKEKQLERDQLIEKIQLGKLQRLV
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    ESMIYYFTKVSSATIEELDLRSELGIPSEF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24831 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25.5%; Score 266.5; DB 2
29.0%; Pred. No. 8.8e-09;
live 55; Mismatches 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   F8B5D6C6618334C8 CRC64;
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05-JUL-2004
05-JUL-2004
05-JUL-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ashbya gossypii (Yeast) (Eremothecium gossypii).
Eukaryota; Fungi; Ascomycota; Saccharomycotina;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AE016816; AAS51172.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=ATCC 10895;
Brachat S., Voegeli S.E.,
Philippsen P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Saccharomycetales; Saccharomycetaceae; Bremothecium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local
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184
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PF03962; Mnd1;
NCE 225 AA;
                                                                                                                                                                                                                                       64 SVEKCGNVNVYWCFKNQLVGKMCTEMQAMKARSEESQVRLQELQAAINSEKKHARAAAFR
                                                                                                                                                                                                                                                                                              61 DCERIGTSNYYWAFPSKALHARKHKLEVLESQLSEGSQKHASLQKSIE-----KAKIGR 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         56;
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                                                                                                                                                                                                                                                                                                                                                                                                         KKKGLSAEEKRTRMMEIFSETKDVFQLKDLEKIAPKE-KGITAMSVKEVLQSLVD-DGMV
                                                                                                                SEGVSYTROALLTEHDELGROLAALOSAYRKLEDTKWDETKIDSYCRGVRSKLEQLDKIT
DNIEVIVSFLMRRHAVSRAELAAALDMPEEFE
                                                         DNIFAIKSWAKRKFGFEENKIDRTFGIPEDFD
                                                                                                                                                                       CETEERTR -- LAKELSSLRDQREQLKAEVEKYKDC -- DPQVVEEIRQANKVAKEAANRWT 170
                                                                                                                                                                                                                                                                                                                                                        KRAVVTLABKKARVLKFFQBEHSIYSIKDLEKLIPKKCAGVSSMLVKDIVQQLIDEDGLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (SEP-2004) to the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25753 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21.1%; Score 221; DB 2;
26.4%; Pred. No. 5.3e-06;
tive 51; Mismatches 93
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Last sequence up
Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BA73C889FFBEB90F CRC64;
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Search completed: July 27, 2005, 09:40:57 Job time: 176 secs

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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                   593.5
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           GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd.
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US-09-914-259-62
US-09-914-259-63
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US-09-914-259-61
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Sequence 4959, Ap
Sequence 14485, A
Sequence 1321, Ap
Sequence 4, Appli
Sequence 55, Appl
Sequence 55, Appl
Sequence 20275, A
Sequence 41, Appl
Sequence 41, Appl
Sequence 708, Appl
Sequence 708, Appl
Sequence 51, Appl
Sequence 20276, A
Sequence 63, Appl
Sequence 64, Appl
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Sequence 16, Appl
Sequence 34, Appl
Sequence 34, Appl
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GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jobert, S.
APPLICANT: Giordano, J.Y.
ITITE OF INVENTION: ESTS and Encoded Human P FILE REFERENCE: GENSET.054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 4959
LENGTH: 127
TYPE: PRT
ORGANISM: Homo sapiens
US-09-621-976-4959

4.

Length 127;

and Encoded Human Proteins

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### ALIGNMENTS

RESULT 1 US-09-621-976-4959

Sequence 4959, App Patent No. 6639063

Application US/09621976

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Sequence 14485, Application US/09248796A
PRICENT NO. 6747137
GENERAL INFORMATION:
APPLICANT: Keith Weinstock et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO AC
TITLE OF INVENTION: FOR DIAGNOSTICS AND THER
FILE REFERENCE: 107196.132
CURRENT FILING DATE: 1999-02-12
PRIOR APPLICATION NUMBER: US/09/248,796A
CURRENT FILING DATE: 1999-02-12
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR FILING DATE: 1998-02-13
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Pred. No. 1.7e-50;
5; Mismatches 2
                                                                                                      AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN AND THERAPEUTICS
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; LOCATION: (0)...(0)
; OTHER INFORMATION: Polypeptide Accession Number Q14203
US-09-538-092-1321
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SOFTWARE: CuraPatSeqFormatter Version
SEQ ID NO 1321
LENGTH: 1270
TYPE: DOT
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PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 14485
LENGTH: 260
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
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Best Local S
                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/538,092
CURRENT FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: 60/127,352
PRIOR FILING DATE: 1999-04-01
PRIOR APPLICATION NUMBER: 60/178,965
PRIOR FILING DATE: 2000-02-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Giot, Loic APPLICANT: Mansfield,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILE REFERENCE: 15966-542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Mansfield, Traci A.
TITLE OF INVENTION: Protein-Protein Complexes
                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
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                              111 KIGRCET--EERTRLAKELSSLRDQREQLKAEVEKYKDCDPQVVEEIRQANKVAKEAANR 168
                                                                                                                                       271 ARKEAKEALEAKERYMEEMADTADAIEMATLDKEMAEERAESLQQEVEALKERVDELTTD
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                                                                     331 LEILKAEIEEKGSDGAASSYQLKQLEEQNARLKDALVRMRDLSSSEKQEHVKLQKLMEK-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 DCERIGTSNYYWAFPSKALHARKHKLEVLESQLSEGSQKHASLQKSIEKAK-----IGR 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       60
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Similarity 27.1%;
59; Conservative 4
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                                                                                                     CERI-----GTSNYYWAFPSKALHAR-KHKLEVLESQLSEGSQKHASLQKSIEKA 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     --FSDSIDDIICYLSRQTGLTMTTLKTEFELPLEFEEI 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NRWIDNIFAIKSWAKRKFGFEENKIDRIFGIPEDFDYI 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CKDETGVRNQTHERASKIRFCDQSLERIDSIQSQLQSLKDSES--VE----NLVTSLAF
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KNQELEVVRQQRERLQEELSQAESTIDELKEQVDAALGAE-EMVEMLTDRNLNLEEKVRE
                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                               12.8%;
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                                                                                                                                                                                                                Score 134.5; |
Pred. No. 0.00
43; Mismatches
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Pred. No. 8.8e-11;
Vigmatches 75;
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tches 106;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Hanson, No. 6232460man D. REGISTRATION NUMBER: 30,946 REFERENCE/DOCKET NUMBER: LUD 54 TELECOMMUNICATION INFORMATION: TELEPHONE: (212) 318-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 25-June-
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/104,324B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Fulbright & Jaworski LLP
STREET: 666 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 08/892,702
FILING DATE: 15-July-1997
ATTORNEY/AGENT INFORMATION:
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OPERATING SYSTEM: PC-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH:
                                                                                                                                                                                                                                  472 QAREKEVHDLEIQLTAITTSEQYYSKEVKDLKTELENEKLKNTELTSHCNKLSLENKELT 531
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650 LESAKOKFGEITDTYOKEIEDKKI
                                      178 -SWAKRKFG------FEENKI 191
                                                                                                                 137 LKAEVEKYKD-CD-----PQVVEEIRQANKVAKE--AANRWTDNIFAIK-----
                                                                                                                                                     532 QETSDMTLELKNQQEDINNNKKQEERMLKQIE--NLQETETQLRNELEYVREELKQKRDE
                                                                                                                                                                                                                                                                                                              413 QKKSSELBEMTKLTNNKEVELEELKKVLGEKETLLYENKQFEKIAEELKG-TEQELIGLL 471
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10103
                                                                          VKCKLDKSEENCNNLRKQVENKNKY I EELQQENKALKKKGTAESKQLNVYE I KVNKLELE
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Methods For Diagnosis And Treating Cancers,
And Methods For Identifying Pathogenic Markers In A Sample
No. 6232460mal Cells
                                                                                                                                                                                                                                                                                                                                                                                                           11.2%; Score 117; DB 3; Length 976; 23.9%; Pred. No. 0.0099;
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RESULT 5

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; TYPE: PRT; ORGANISM: Sus scrofa US-09-914-259-55
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                                                                                                           APPLICANT: Hyman, Paul
APPLICANT: Williams, Mark
APPLICANT: Williams, Mark
TITLE OF INVENTION: STAGED ASSEMBLY OF NANOSTRUCTURES
FILE REFERENCE: 8471-010-999
CURRENT FILING NUMBER: US/09/914,259
CURRENT FILING DATE: 2000-11-21
NUMBER OF SEQ ID NOS: 180
SOPTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 55
LENGTH: 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 1387
SOFTWARE: CuraPatSegFormatter Version
SEQ ID NO 1339
                                                                                                                                                                                                                                                                                                                                          Sequence 55, Appli
Patent No. 6495336
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Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
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CURRENT APPLICATION NUMBER: US/09/538,092
CURRENT FILING DATE: 2000-03-29
RRIOR APPLICATION NUMBER: 60/127,352
PRIOR FILING DATE: 1999-04-01
PRIOR APPLICATION NUMBER: 60/178,965
PRIOR APPLICATION NUMBER: 60/178,965
PRIOR FILING DATE: 2000-02-01
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APPLICANT: Mansfield, Traci A.
TITLE OF INVENTION: Protein-Protein Complexes and Method
                                                                                                                                                                                                                                                                                                       APPLICANT: Makowski,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
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LOCATION: (0)...(0)
OTHER INFORMATION: Polypeptide Accession Number Q15431
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                                                                                                                                                                                                                                                                                                       Lee
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 10.9%;
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Pred. No. 0.0099
 Score 114; DB 4;
Pred. No. 0.0037;
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                   Length 284;
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US-09-248-796A-20275
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US-09-914-259-62
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Sequence 20275, Application US/09248796A
PATERIX NO. 6747137
GENERRAL INFORMATION:
APPLICANT: Keith Weinstock et al
APPLICANT: Keith Weinstock et al
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
TILE REFERENCE: 107196.132
CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT FILING DATE: 1999-02-12
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR FILING DATE: 1998-02-13
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Patent No. 6495336
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CURRENT APPLICATION NUMBER: US/09/914,259
CURRENT FILING DATE: 2000-11-21
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APPLICANT: Hyman, Paul
APPLICANT: Williams, Mark
TITLE OF INVENTION: STAGED ASSEMBLY OF NANOSTRUCTURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       104 ---ERLATALQKLEEAEKAADESERGMKVIESRAQKDEEKMEIQEIQLKEAKHIAEDADR 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              164 EVARKLVIIESDLERAEERAELSEGKC-----AELEEELKTVTNNLKSLEAQAEKYSQKE 218
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              58 ---GMVDCERIGTSNYYWAFPSKALHAR----XHKLEVLESQLSEGSQKH-------
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RESULT 10
US-09-538-092-918
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US-09-914-259-43
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PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 20275
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SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 43
LENGTH: 284
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Best Local S
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Best Local :
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APPLICANT: Hyman, Paul
APPLICANT: Williams, Mark
TITLE OF INVENTION: STAGED ASSEMBLY OF NANOSTRUCTURES
FILE REFERENCE: 8471-010-999
CURRENT APPLICATION NUMBER: US/09/914,259
CURRENT FILING DATE: 2000-11-21
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TYPE: PRT
ORGANISM: Candida albicans
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ORGANISM: Homo
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Local Similarity 23.8%;
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52; Conserv
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                                                                                                          KVAKEAANRWTDNIFAIKSWAKRKFGFEENKIDRTFGIPED 200
                                                                                                                                                                                EKAKIGRCETEERTRLA-----KELSSLRDQREQLKAEVEKYKDCDPQVVEEIRQAN 159
                                                                                                                                                                                                                                                                                             LAEKKAADAEAEVASINRRIQLVEEELDRAQERLATALQKLEEAEKAADESERGMKVIEN 132
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                                                                                                                                                ER-----TEERAELAESKCSELEEELKNVTNNLKSLEAQAEKYSQKEDKYEEEIKILT
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                                                                                                                                                                                                                                                                                                                                                                       41; Mismatches
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CURRENT APPLICATION NUMBER: US/09/914,259
CURRENT FILING DATE: 2000-11-21
NUMBER OF SEQ ID NOS: 180
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 46
LENGTH: 284
TYPE: PRT
ORGANISM: Brachydanio rerio
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US-09-914-259-46
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                                                                           Matches
                                                                                                Best Local
                                                                                                              Query Match
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CURRENT APPLICATION NUMBER: US/09/538,092
CURRENT FILING DATE: 2000-03-29
                                                                                                                                                                                                                                                                                                                           APPLICANT: Makowski, Lee
APPLICANT: Hyman, Paul
APPLICANT: Williams, Mark
TITLE OF INVENTION: STAGED ASSEMBLY OF NANOSTRUCTURES
FILE REFERENCE: 8471-010-999
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PRIOR FILING DATE: 1999-04-01
PRIOR APPLICATION NUMBER: 60/178,965
PRIOR FILING DATE: 2000-02-01
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ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
LOCATION: (0)...(0)
OTHER INFORMATION: Polypeptide Accession Number P13535
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1476 ESRSISTELFKVKNVYEESIDQLETIRRENKNIQQEISDLTEQIAEGGKQIHELEKIKKQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                141 VEKYKDCDPQVVEEIRQANKVAKEA-ANRWTDNIFAIKSWAKRKFGFEENKIDR 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99 KHASLQKSIEKAK-----IGRCET--EERTRLAKELSSLRDQ-----REQLKAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    48 KEVLQSLVDDGMVDCERIGTS------NYYWAFPSKALHARKHKLEVLESQLSEGSQ 98
   73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 KKGLSAEEKRTRMMEIFSETKDVFQLKDLEKIAPK-----EKGITAMS-----V 47
                                     1 MSKKKGLSAE---EKRTRMMEIFSETKDVFQ------LKDLEKIAPK-EKGITAMSV 47
                                                                                              Similarity
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Conservative
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                                                                                            10.5%;
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23.1%; Pred. No. 0.096;
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                                                                         44;
                                                                         Score 110; DB 4;
Pred. No. 0.0092;
14; Mismatches 72;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 4; Length 1937;
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                                                                                                                Length 284;
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US-09-438-185A-708
; Sequence 708, Application US/09438185A
; Patent No. 6822071
APPLICANT: Stephens, Richard
APPLICANT: Mitchell, Wayne
APPLICANT: Kalman, Sue
APPLICANT: Kalman, Sue
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: Chlamydia Pneumoniae Genome Sequence
FILE REFERENCE: 018941-000411US
CURRENT APPLICATION NUMBER: US/09/438,185A
CURRENT FILING DATE: 2002-03-13
PRIOR APPLICATION NUMBER: US 60/108,279
PRIOR APPLICATION NUMBER: US 60/108,606
PRIOR APPLICATION NUMBER: US 60/128,606
PRIOR APPLICATION NUMBER: US 60/128,606
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LENGTH: 284
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GENERAL INFORMATION:
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Best Local (
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APPLICANT: Hyman, Paul
APPLICANT: Williams, Mark
TITLE OF INVENTION: STACED ASSEMBLY OF NANOSTRUCTURES
FILE REFERENCE: 8471-010-999
CURRENT APPLICATION NUMBER: US/09/914,259
CURRENT FILLING DATE: 2000-11-21
NUMBER OF SEQ ID NOS: 180
SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ANRWIDNIFAIKSWAKRKFGFEENKID 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ERAE-ERAELSESKCAELEEELKTVTNNLKSLEAQAEKYSQKEDKYEEEIKVLTDKLKEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EKAKIGRCETEER--TRLAKELSSLRDQREQLKAEVEKYKDCDPQVVEEIRQANKVAKEA 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R----ALKDEEKIELQEI------QLKEAKHIAEEADRKYEEVARKLVIIEGDL
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                                                                                                                                                                                                                                                                                                                                                                                                                                254
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RESULT 15
US-09-248-796A-20276
; Sequence 20276, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Makowski, Lee
APPLICANT: Hyman, Paul
APPLICANT: Williams, Mark
TITLE OF INVENTION: STAGED ASSEMBLY OF NANOSTRUCTURES
FILE REFERENCE: 8471-010-999
CURRENT APPLICATION NUMBER: US/09/914,259
CURRENT FILING DATE: 2000-11-21
NUMBER OF SEQ ID NOS: 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 51
LENGTH: 284
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SOFTWARE: FeatSEQ for Windows Version 3.0
SEO ID NO 708
LENGTH: 170
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Matches 48; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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OTHER INFORMATION: CPn0706
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                        49;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          71 -----SDAVLQIKSYIKVVAVQLSEEEEKVNKQKEVVLAASKELEKAEVNLAKRRKEEE
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                                                                                                                                                                                                                                                                                                                                              73 LSDKKATDAEGDVASLNRRIQLVEEELDRAQERLSTALQKLEEAEKAADESERGMKVIEN 132
                                                                                                                                                                                                                                                                                                                                                                                  1 MSKKKGLSAE---EKRTRMMEIFSETKDVFQ-----LKDLEKIAPK-EKGITAMSV 47
                                                                                                                                                                ANRWIDNIFAIKSWAKRKFGFEENKID 192
                                                                                                                                                                                                ETR-----AEFAERTVAKLEKSID
                                                                                                                                                                                                                                    EKAKIGRCETEER--TRLAKELSSLRDQREQLKAEVEKYKDCDPQVVBEIRQANKVAKEA 165
                                                                                                                                                                                                                                                                        R----ALKDEEKMELQEI------QLKEAKHIAEEADRKYEEVARKLVIIEGDL
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                                                                                                                                                                                                                                                                                                                                                                                                                      37; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 109; DB 4
Pred. No. 0.011;
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APPLICANT: Keith Weinstock et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.132
CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT FILING DATE: 1999-02-12
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR FILING DATE: 1998-02-13
PRIOR FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 20276
LENGTH: 817
TYPE: PRT
ORGANISM: Candida albicans
US-09-248-796A-20276
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Search completed: July 27, 2005, 09:42:31 Job time : 43 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 10.3%; Score 108; DB 4; Length 817; Best Local Similarity 24.4%; Pred. No. 0.059; Matches 49; Conservative 43; Mismatches 85; Indels 3
                                                                                                                                            179 WAKRKFGFEENKIDRTFGIPE 199
                                                                                                                                                                                             9 AEEKRTRMMEIFSETKDVFQLKDLEKIAPKEKGITAMSVK--EVLQSLVD---DGMVDCE 63 ||||: ::: | :| :| :| :| :| | :| 426 AEEKQV-LLDEKKENQDRIDTEEAEKIAARKQELEELQAEKDEILKPTLDELKEESAKLE 484
                                                                                                599 KVK-----DEHKINSE--LPE 612
                                                                                                                                                                                                                                                                                                485 EVTNARDELANEVKASEDLNKEYEEKLAELESKLQEAKNDIEKYTTDIEEA-----TAK 538
                                                                                                                                                                                                                                                                                                                                     64 RIGTSNYYWAFPSKALH----ARKHKLEVLESQLSEGSQKHASLQKSIEKAKIGRCETEE 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              85; Indels 24; Gaps
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Result
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Maximum DB seq length: 200000000
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Maximum Match 10
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Scoring table:
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                                                                                                                                                                                                                                                                                                                                                                  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                Score
                                                                                                                                                                                                 1047
1047
        Match
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/ Cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
/ Cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
/ Cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
/ Cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
/ Cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
/ Cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
/ Cgn2_6/ptodata/1/pubpaa/US108_PUBCOMB.pep:*
/ Cgn2_6/ptodata/1/pubpaa/US108_PUB.pep:*
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/ Cgn2_6/ptodata/1/pubpaa/US108_PUB.pep:*
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Copyright (c) 1993 - 2005 Compugen Ltd.
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        100%
    US-09-799-250-2
US-10-087-190-3
US-110-087-190-14
US-10-087-190-20
US-10-087-190-21
US-10-087-190-61
US-10-087-190-61
US-10-087-190-44
US-10-087-190-45
US-10-087-190-45
US-10-087-190-45
US-10-087-190-24
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511.176 Million cell updates/sec
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Sequence 2, Appli
Sequence 1, Appli
Sequence 14, Appl
Sequence 20, Appl
Sequence 21, Appl
Sequence 22, Appl
Sequence 61, Appl
Sequence 44, Appl
Sequence 44, Appl
Sequence 45, Appl
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45	44	43	42	41	40	39	38	37	36	35	34	3	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12
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10-732-923-33	-09-981-151A-48	-10-032-585-7646	-10-408-765A-20	9-1926	-10-083-357-13	-10-106-698-544	-10-087-190-	-09-799-250-	-437-963-16290	-10-437-963-1	-10-425-115-25301	-10-087-190-	-10-087-190-1	-10-087-190-	-10-087-19	-10-087-190-	-10-087-190-	-10-087-190-5	-10-087-190-5	-10-087-190-	-10-087-190-	-087-190-5	-10-087-190-	-10-087-190-6	-10-087-190-1	-10-087-190-1	-10-087-190-	-09-799-250-	-10-087-190-6	-10-087-190-	-087-190-6	-10-087-190-	US-10-087-190-13
equence 3300	æ	equence 7646	e 2096	equence 19:	equence	e 54	e 25								Sequence 47, Appl						O	e 53	e 63	æ	e 18,	equence 11,	e 23,	e 4,	e 69,	e 68,	equence 67,	equence 19,	Sequence 13, Appl

### ALIGNMENTS

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CURRENT APPLICATION NUMBER: US/09/799,250
CURRENT FILING DATE: 2001-02-08
NUMBER OF SEQ ID NOS: 719
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
SEQ ID NO 2
LENGTH: 205
TYPE: PRT
ORGANISM: Homo sapiens
US-09-799-250-2
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US-09-799-250-2
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APPLICANT: Fia M. Challita-Eid
APPLICANT: Rene S. Hubert
APPLICANT: Steve Chappell Mitchell
APPLICANT: Arthur B. Raitano
APPLICANT: Arthur B. Raitano
                                                                                                                              Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 205; Conservative 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Aya Jakobovits
TITLE OF INVENTION: 121P1F1: A TISSUE SPECIFIC PROTEIN
TITLE OF INVENTION: HIGHLY EXPRESSED IN VARIOUS CANCERS
FILE REFERENCE: 129.34US01
61 DCERIGTSNYYWAFPSKALHARKHKLEVLESQLSEGSQKHASLQKSIEKAKIGRCETEER 120
                                                                    1 MSKKKGLSAEEKRTRMEIFSETKDVFQLKDLEKIAPKEKGITAMSVKEVLQSLVDDGMV
                                           MSKKKGLSAEEKRTRMMEIFSETKDVFQLKDLEKIAPKEKGITAMSVKEVLQSLVDDGMV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mary Faris
Daniel E.H. Afar
                                                                                                                              ; Score 1047; DB 10; Pred. No. 3.8e-78; 0; Mismatches 0;
                                                                                                                                                                     DB 10;
                                                                                                                                                                          Length
                                                                                                                              0;
                                                                                                                              Gaps
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1047 1036.5 1036.5 1011

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APPLICANT: Afar, Daniel E. H.
APPLICANT: Ge, Wangmao
APPLICANT: Jakobovitz, Aya
TITLE GF, WANGMAO
APPLICANT: Jakobovitz, Aya
TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
TITLE OF INVENTION: ENTITLED 121P1F1 USEFUL IN TREATMENT AND DETECTION OF CANCER
FILE REFERENCE: 51158-20034.20
CURRENT APPLICATION NUMBER: US/10/087,190
CURRENT FILING DATE: 2003-01-28
PRIOR APPLICATION NUMBER: US 09/779,250
PRIOR APPLICATION NUMBER: US 09/779,250
PRIOR APPLICATION NUMBER: US 09/779,250
PRIOR FILING DATE: 2001-03-05
NUMBER OF SEQ ID NO3: 69
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 205
TYPE: PRT
ORGANISM: Homo Sapiens
US-10-087-190-3
Sequence 14, Application US/10087190
Publication No. US20030223997A1
GENERAL INFORMATION:
APPLICANT: Agensys, Inc.
APPLICANT: Challita-Eid, Pia M.
APPLICANT: Hubert, Rene S.
APPLICANT: Raitano, Arthur B.
APPLICANT: Faris, Mary
APPLICANT: Afar, Daniel E. H.
APPLICANT: Ge, Wangmao
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APPLICANT: Agensys, Inc.,
APPLICANT: Challita-Eid, I
APPLICANT: Hubert, Rene S,
APPLICANT: Raitano, Arthu
APPLICANT: Faris, Mary
APPLICANT: Afar, Daniel E,
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Matches 205;
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Afar, Daniel E. H.
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Conservative (
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Arthur B.
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Pred. No. 3.8e-78;
Mismatches 0;
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; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-087-190-14
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                                                                                                                                                     ; TYPE: PRT ; ORGANISM: Homo Sapiens US-10-087-190-20
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US-10-087-190-20
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TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
TITLE OF INVENTION: ENTITLED 121P1F1 USEFUL IN TREATMENT AND DETECTION
TITLE OF INVENTION: ENTITLED 121P1F1 USEFUL IN TREATMENT AND DETECTION
CURRENT FILING DATE: 2003-01-28
PRIOR APPLICATION NUMBER: US 09/779,250
PRIOR FILING DATE: 2001-03-05
NUMBER OF SEQ ID NOS: 69
SOPTWARE: FRRESEQ for Windows Version 4.0
SEQ ID NO 14
SECOTOR OF SEQ ID NOS: 69
SEQ ID NO 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 100.0%; Score 1047; DB 15
Best Local Similarity 100.0%; Pred. No. 3.8e-78;
Matches 205; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 20, Application US/10087190 Publication No. US20030223997A1
                                                                             Matches
                                                                                                                                                                                                                                 SEQ ID NO 20
                                                                                                                 Query Match
                                                                                                                                                                                                                                                                               APPLICANT: Jakobovitz, Aya
TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
TITLE OF INVENTION: ENTITLED 121P1F1 USEFUL IN TREATMENT F
FILE REFERENCE: 51158-20034.20
CURRENT APPLICATION NUMBER: US/10/087,190
CURRENT FILING DATE: 2003-01-28
PRIOR APPLICATION NUMBER: US 09/779,250
PRIOR FILING DATE: 2001-03-05
PRIOR FILING DATE: 2001-03-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Challita-Eid, FAPPLICANT: Hubert, Rene S. APPLICANT: Raitano, Arthur
                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 69
SOFTWARE: FastSEQ for Windows
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Agensys, Inc. APPLICANT: Challita-Eid,
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                                                                                                                                                                                                             LENGTH: 205
                                                                                               Local
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Afar, Daniel E. H.
Ge, Wangmao
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                   MSKKKGLSAEEKRTRMMEIFSETKDVFQLKDLEKIAPKEKGITAMSVKEVLQSLVDDGMV
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MSKKKGLSAEEKRTRMMEIFSETKDVFQLKDLEKIAPKEKGITAMSVKEVLQSLVDDGMV
                                                                         100.0%; Score 1047; DB 15; ilarity 100.0%; Pred. No. 3.8e-78; Conservative 0; Mismatches 0;
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Sequence 22, Application US/10087190
Publication No. US/20030223997A1
GENERAL INFORMATION:
APPLICANT: Agensys, Inc.
APPLICANT: Challita-Eid, Pia M.
APPLICANT: Hubert, Rene S.
APPLICANT: Raitano, Arthur B.
APPLICANT: Faris, Mary
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US-10-087-190-22
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US-10-087-190-21
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Best Local S
Matches 205
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TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
TITLE OF INVENTION: ENTITLED 121P1F1 USEFUL IN TREATMENT AND DETECTION OF
FILE REFERENCE: 51158-20034.20
CURRENT FILING DATE: 2003-01-28
PRIOR APPLICATION NUMBER: US/10/087,190
PRIOR APPLICATION NUMBER: US 09/779,250
PRIOR FILING DATE: 2001-03-05
NUMBER OF SEQ ID NOS: 69
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 21
LENGTH: 2005
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ORGANISM: Homo Sapiens
-10-087-190-21
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APPLICANT: Challita-Eic
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Local Similarity 100.0%; Pred. No. 3.8e-78;
nes 205; Conservative 0; Mismatches 0;
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Raitano, Arthur B.
Faris, Mary
Afar, Daniel E. H.
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Hubert, Rene S.
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Afar, Daniel E. H.
Ge, Wangmao
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; TYPE: PRT
; ORGANISM: Homo
US-10-087-190-61
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US-10-087-190-61
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APPLICANT: Jakobovitz, Aya

TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN

TITLE OF INVENTION: ENTITLED 12191F1 USEFUL IN TREATMENT AND DETECTION OF CANCER

FILE REFERENCE: 51158-20034.20

CURRENT APPLICATION NUMBER: US/10/087,190

CURRENT FILING DATE: 2003-01-28

PRIOR APPLICATION UNMEER: US 09/779,250

PRIOR FILING DATE: 2001-03-05

NUMBER OF SEQ ID NOS: 69

SOFTMARE: FastSEQ for Windows Version 4.0

SEQ ID NO 61

LENGTH: 205
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APPLICANT: Challita-Eid, Pia M.
APPLICANT: Hubert, Rene S.
APPLICANT: Raitano, Arthur B.
APPLICANT: Faris, Mary
APPLICANT: Afar, Daniel E. H.
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APPLICANT: Jakobovitz, Aya
APPLICANT: Jakobovitz, Aya
TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
TITLE OF INVENTION: ENTITLED 121P1F1 USEFUL IN TREATMENT AND DETECTION OF CANCER
TITLE REFERENCE: 51158-20034.20
CURRENT APPLICATION NUMBER: US/10/087,190
CURRENT FILING DATE: 2003-01-28
PRIOR APPLICATION NUMBER: US 09/779,250
PRIOR APPLICATION NUMBER: US 09/779,250
PRIOR TILING DATE: 2001-03-05
NUMBER OF SEQ ID NOS: 69
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 22
LENGTH: 205
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Matches
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Best Local Similarity 100.0%; F
Matches 205; Conservative 0;
                                                                                                                                  Query Match
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ORGANISM: Homo
                                                                                                            Local Similarity
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                      MSKXKGLSAEEKRTRMMEIFSETKDVFQLKDLEKIAPKEKGITAMSVKEVLQSLVDDGMV
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MSKKKGLSAEEKRTRMME1FSETKDVFQLKDLEK1APKEKG1TAMSVKEVLQSLVDDGMV
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                                                                                   100.0%; Score 1047; DB 15; ilarity 100.0%; Pred. No. 3.8e-78; Conservative 0; Mismatches 0;
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Pred. No. 3.8e-78;
Pred. No. 3.8e-78;
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Sequence 44, Application US/10087190
Publication No. US20030223997A1
GENERAL INFORMATION:
APPLICANT: Agensys, Inc.
APPLICANT: Challita-Eid, pia M.
APPLICANT: Hubert, Rene S.
APPLICANT: Raitano, Arthur B.
APPLICANT: Raitano, Arthur B.
APPLICANT: Afar, Daniel E. H.
APPLICANT: Afar, Daniel E. H.
APPLICANT: Ge, Wangmao
APPLICANT: Ge, Wangmao
APPLICANT: Jakobovitz, Aya
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US-10-408-765A-1821
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; ORGANISM: Homo sapiens
US-10-408-765A-1821
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CURRENT APPLICATION NUMBER: US/10/408,765A
CURRENT FILING DATE: 2003-04-04
NUMBER OF SEQ ID NOS: 3077
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1821
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Best Local Similarity
Matches 205; Conserv
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APPLICANT: Taylor, Steven w.
APPLICANT: Glenn, Gary M.
APPLICANT: Warnock, Dale E.
TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
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APPLICANT: Fahy, Eoin D.
APPLICANT: Zhang, Bing
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                                                                                                                                                                                                                                                                                                              KRKFGFEENKIDRTFGIPEDFDYID 205
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100.0%; Pred. No. 3.8e-78;
vative 0; Mismatches 0;
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Sequence 45, Application US/10087190
Publication No. US20030223997A1
GENERAL INFORMATION:
APPLICANT: Agensys, Inc.
APPLICANT: Challita-Eid, Pia M.
APPLICANT: Hubert, Rene S.
APPLICANT: Raitano, Arthur B.
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US-10-087-190-45
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US-10-087-190-44
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                                                                                                                                                                                             ; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-087-190-45
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TITLE OF INVENTION: ENTITLED 121P1F1 USEFUL IN TREATMENT AND DETECTION OF CANCER
FILE REFERENCE: 51158-20034.20
CURRENT APPLICATION NUMBER: US/10/087,190
CURRENT FILING DATE: 2003-01-28
PRIOR APPLICATION NUMBER: US 09/779,250
PRIOR APPLICATION NUMBER: US 09/779,250
PRIOR FILING DATE: 2001-03-05
NUMBER OF SEQ ID NOS: 69
SOPTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 44
LENGTH: 206
TYPE: PRT
                                                                                                                    Best Loc
Matches
                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 69
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 45
LENGTH: 206
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Best Local Similarity
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APPLICANT: Jakobovitz, Aya
APPLICANT: Jakobovitz, Aya
TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
TITLE OF INVENTION: ENTITLED 121P1F1 USEFUL IN TREATMENT AND DETECTION OF CANCER
FILE REFERENCE: 51158-20034.20
CURRENT APPLICATION NUMBER: US(10/087,190
CURRENT FILING DATE: 2003-01-28
PRIOR APPLICATION NUMBER: US 09/779,250
PRIOR FILING DATE: 2001-03-05
PRIOR FILING DATE: 201-03-05
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APPLICANT: Afar, Daniel E. H.
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Local Similarity 99.5%;
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                                                           MSKKKGLSAEEKRTRMMEIFSETKDVFQLKDLEKIAPKEKGITAMSVKEVLQSLVDDGMV
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    DCERIGTSNYYWAFPSKALHARKHKLEVLESQ-LSEGSQKHASLQKSIEKAKIGRCETEE 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AKRKFGFEENKIDRTFGIPEDFDYID
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                                      MSKKKGLSAEEKRTRMMEIFSETKDVFQLKDLEKIAPKEKGITAMSVKEVLQSLVDDGMV
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Pred. No. 2.8e
0; Mismatches
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Pred. No. 2.8e
0; Mismatches
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es 0; Indels
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PRIOR APPLICATION NUMBER: US 09/779,250
PRIOR FILING DATE: 2001-03-05
NUMBER OF SEQ ID NOS: 69
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 24
LENGTH: 198
TYPE: PRT
ORGANISM: Homo Sapiens
US-10-087-190-24
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US-10-087-190-13
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US-10-087-190-24
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                                                    Sequence 13, Application US/10087190
Publication No. US20030223997A1
GENERAL INFORMATION:
APPLICANT: Agensys, Inc.
APPLICANT: Challita-Eid, Pia M.
APPLICANT: Hubert, Rene S.
APPLICANT: Raitano, Arthur B.
APPLICANT: Raitano, Arthur B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 96.6%; Score 1011; DB 15; Best Local Similarity 100.0%; Pred. No. 3.3e-75; Matches 198; Conservative 0; Mismatches 0;
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TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
TITLE OF INVENTION: ENTITLED 121P1F1 USEFUL IN TREATMENT AND DETECTION OF CANCER
FILE REFERENCE: 51158-20034.20
CURRENT APPLICATION NUMBER: US/10/087,190
CURRENT FILING DATE: 2003-01-28
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                                     APPLICANT:
                      APPLICANT:
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                                                                                                                                                                                                                                                                                        GFEENKIDRTFGIPEDFD 202
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Faris, Mary
Afar, Daniel E. H.
Ge, Wangmao
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Afar, Daniel E. H.
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APPLICANT: Jakobovitz, Aya
TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
TITLE OF INVENTION: ENTITLED 121P1F1 USEFUL IN TREATMENT AND
FILE REFERENCE: 51158-20034.20
CURRENT APPLICATION NUMBER: US/10/087,190
CURRENT FILING DATE: 2003-01-28
PRIOR APPLICATION NUMBER: US 09/779,250
PRIOR FILING DATE: 2001-03-05
INUMBER OF SEQ ID NOS: 69
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 19
LENGTH: 190
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; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
; TITLE OF INVENTION: ENTITLED 121P1F1 USEFUL IN TREATMENT AND
; FILE REFERENCE: 51188-20034.20
; CURRENT APPLICATION NUMBER: US/10/087,190
; CURRENT FILING DATE: 2003-01-28
; PRIOR APPLICATION NUMBER: US 09/779,250
; PRIOR FILING DATE: 2001-03-05
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 190
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US-10-087-190-19
; Sequence 19, Application US/10087190
; Publication No. US20030223997A1
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; ORGANISM: Homo
US-10-087-190-13
                                                                                                                                                 US-10-087-190-19
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Best Local Similarity
                                                                           Matches
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                                                                                                          Query Match
                                                                                             Best Local Similarity
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APPLICANT:
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APPLICANT: Challita-Eid, P.
APPLICANT: Hubert, Rene S.
APPLICANT: Raitano, Arthur
                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Faris, Mary APPLICANT: Afar, Daniel E. H.
                                                                                                                                                                 TYPE: PRT
ORGANISM: Homo
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61 SKALHARKHKLEVLESQLSEGSQKHASLQKSIEKAKIGRCETEERTRLAKELSSLRDQRE
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                                                                           Conservative
                                                                                                                                                                   Sapiens
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                                                                       93.1%; Score 975; DB 15;
100.0%; Pred. No. 2.9e-72;
tive 0; Mismatches 0;
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Sequence 68, Application US/10087190
Publication No. US20030223997A1
GENERAL INFORMATION:
APPLICANT: Ageneys, Inc.
APPLICANT: Challita-Eid, Pia M.
APPLICANT: Hubert, Rene S.
APPLICANT: Hubert, Rene S.
APPLICANT: Raitano, Arthur B.
APPLICANT: Faris, Mary
APPLICANT: Afar, Daniel E. H.
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US-10-087-190-67
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Best Local S
Matches 190
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TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
TITLE OF INVENTION: ENTITLED 121P1F1 USEFUL IN TREATMENT AND DETECTION OF CANCER
TILE REFERENCE: $11.58-20034.20
CURRENT PILING DATE: 2003-01-28
PRIOR APPLICATION NUMBER: U$/10/087,190
CURRENT FILING DATE: 2003-01-28
PRIOR FILING DATE: 2001-03-05
PRIOR FILING DATE: 2001-03-05
NUMBER OF SEQ ID NOS: 69
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 67
LENGTH: 190
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APPLICANT: Challita-Eid, Pia M
APPLICANT: Hubert, Rene S.
APPLICANT: Raitano, Arthur B.
APPLICANT: Faris, Mary
APPLICANT: Afar, Daniel E. H.
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Publication No.
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ORGANISM: Homo Sapiens
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Afar, Daniel E. H.
Ge, Wangmao
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Faris, Mary
Afar, Daniel E. H.
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; APPLICANT: Ge, Wangmao
; APPLICANT: Jakobovitz, Aya
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN
; TITLE OF INVENTION: ENTITLED 121P1F1 USEFUL IN TREATMENT AND
; FILE REFERENCE: 51158-20034.20
; CURRENT APPLICATION NUMBER: US/10/087,190
; CURRENT FILING DATE: 2003-01-28
; PRIOR APPLICATION NUMBER: US 09/779,250
; PRIOR FILING DATE: 2001-03-05
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 68
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Search completed: July 27, 2005, 09:54:35 Job time : 157 secs
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